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GenCore version 5.1.8
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protein - protein search, using sw model

Run on:

May 19, 2006, 17:34:57; Search time 158.667 Seconds (without alignments) 391.900 Million cell updates/sec

US-09-889-936A-6 737 Perfect

1 MRVLILLWLFTAFPGILSDV.......wDYGTTYGYFDVWGQGTTVT 136 score:

Scoring table: Sequence:

2589679 segs, 457216429 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

2589679 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_8:* Database :

geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2006s: geneseqp20048:* geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IES	Description		Aab15672 Murine 5B	Ady91369 Anti-KID3	Adz81889 Anti-lami	Aee98109 Murine PE	Aaw01144 MAb 1.4 h	Aaw44169 Monoclona	Aar28671 pPM-h1 pr	Abb82796 Antibody	Ads14282 Murine pr	Ads14288 Murine pr	Ado44274 Consensus		Adj76886 Anti-IGF-	Adz67056 Murine im	Aee61302 Murine mo	Ado44272 Primer in	Ado44280 Humanised		Abp59986 Antibody	Adf69650 Humanised	Aeb03869 B-CLL pha	Aee17798 Anti-huma	Aaw01584 Lead bind
SUMMARIES	e E		AAB15672	ADY91369	ADZ81889	AEE98109	AAW01144	AAW44169	AAR28671	ABB82796	ADS14282	ADS14288	AD044274	AD044271	ADJ76886	ADZ67056	AEE61302	AD044272	AD044280	ADL26964	ABP59986	ADF69650	AEB03869	AEE17798	AAW01584
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	* Query Match		100.0	85.1	84.5	80.5	79.9	79.9	79.8	79.6	77.3	77.3	75.5	75.5	75.2	75.2	75.2	75.0	73.9	73.9	73.8	73.8	73.8	73.8	73.4
	Score		737	627.5	622.5	593.5	588.5	588.5	588	586.5	569.5	569.5	556.5	556.5	554	554	554	552.5	544.5	544.5	544	544	544	544	541
	Result No.	1	н	8	e	4	2	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

Aec08410 ScFv-B2-F Aec08411 ScFv-B2-F Aec08409 ScFv-A12A Aec08408 ScFv-A12A		Aec20775 M-CSF spe Adj80371 Murine an Adz81874 Anti-lami Adw14662 Anti-comp Aar24722 Sequence Aec27772 M-CSF spe	M-CSF Anti- Mouse Murin Mouse Antib
AEC08410 AEC08411 AEC08409	AEE17974 AAW21937 AAY05267 ABG98318 ADR42630	AEC20775 ADJ80371 ADZ81874 ADW14662 AAR24722 AEC20767	AEC20763 ADJ76904 ADZ67074 AEE61320 ADZ81898 ADU39968 AAR07318
730 9 761 9 761 9			1118 9 1118 9 1118 9 1114 9 1117 8
73.2	72.27 72.27 72.27 72.4	72.3 72.3 72.1 71.8	71.7 71.6 71.6 71.6 71.4 71.4
24 539.5 25 539.5 26 539.5 27 539.5		533	330 520 641 641 627 643 644 644 656 667 667 667 667 667 667 667

ALIGNMENTS

Mouse; 5B3 antibody; IgG1; piezoelectric immunoassay; small molecule explosive detection; 2,4,6-trinitrotoluene; TNT. Murine 5B3 antibody heavy chain variable region. AAB15672 standard; protein; 136 AA (first entry) WO200043774-A2. 08-JAN-2001 AAB15672; Mus sp. RESULT 1 AAB15672

25-JAN-2000; 2000WO-IL000048. 99IL-00128212 25-JAN-1999; 27-JUL-2000.

(YISS) YISSUM RES & DEV CO. (YEDA) YEDA RES & DEV CO LTD.

Willner I, Eshhar Z;

WPI; 2000-524259/47. N-PSDB; AAA74604.

Apparatus for detecting small molecules, especially explosives comprises a piezoelectric crystal.

Disclosure; Fig 3A; 90pp; English.

The present sequence is the heavy chain variable region of 5B3 antibody. The CDNA encoding this sequence was obtained from total RNA extracted from a 5B3 hybridoma by RT-PCR. 5B3 is an igg1 antibody derived from a TNP-KLH immunised mouse. Its binding to TNP or DNS antigen can be blocked by very low amounts of TNT and it can therefore be used in a method for a detecting small assayed explosive molecules. Molecules are detected using a piezoelectric sensor. Piezoelectric immunoassaying in liquid phase allows stationary and flow analysis of an aqueous sample. The method is sufficiently sensitive for detection of low molecular weight molecules

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antibody therapy; diagnosis; cancer; neoplasm; cytostatic; sarcoma; dermacological disease; tumor; bladder tumor; genitourinary disease; bone tumor; musculoskeletal disease; osteogarcoma; brain tumor; neurological disease; breast tumor; endocrine disease; sprecology and obsterrics; colon tumor; gastrointestinal disease; hematological disease; hematological disease; liver tumor; hepatocellular carcinoma; lumboma; immune disorder; lung tumor; respiratory disease; melanoma; humbiple myeloma; myeloday myeloma; syndrome; immunostimulant; ovary tumor; endocrine disease; parathyroid tumor; prostate tumor; andrology; skin tumor; stomach tumor; uterine cervix tumor;
                                                                                                                                                                                                                                                                                                               61 GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYG 120
                                                                                                                                                                                                                                                                                                                                                                             61 GNKLEWMGYISYSGFTSYNPSLRSFTRDTSKNOFFLOLNSVTSEDTATYYCARWDYG 120
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                                                                                                                                                                                      1 MRVLILLWLFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFP
                                                                                                                           Gaps
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                                                          Length 136;
                                                                                                                        Indels
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139. .468
/note= "Human Gl constant region"
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                                                             100.0%; Score 737; DB 3; 100.0%; Pred. No. 5.2e-61;
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                                                                                                                        0; Mismatches
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                                                                                                                     Matches 136; Conservative
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                                                             Query Match
Best Local Similarity
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Sequence 136 AA;
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ID ADY91369
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various human cancers, and diseases that express KID3, e.g. leukemias, breast cancer.

8; 96pp; English. Disclosure; Fig

CC The invention or islates to a substantially puritied immunoglobuling characteristics: the shility to bind to KID3 on a concert cell in the ability to bind to KID3 on a concert cell; the ability to bind to KID3 on a concert cell; the ability to bind to KID3 on a concert cell; the ability to bind to KID3 on a concert cell; the ability to bind to KID3 on a concert cell; the ability to deliver a therapeutic agent or detectable marker into cell; the ability to deliver a therapeutic agent or detectable marker into a cancer cell expressing KID3. Also included are an isolated muclaic acid sequence coding for the immunoglobulin polypeptide (or its epitope binding fragment,) a cancer cell interpreted coding a cancer cell interpreted caid under conditions in growing a cell line transfermed with the muclaic acid under conditions in change a cancer cell interpreted coding a cell line transfermed with the muclaic acid under conditions in communoglobulin polypeptide (or its epitope binding fragment is a pharmaceutical composition (comprising a therapeutical) with the immunoglobulin polypeptide or epitope binding fragment is a pharmaceutical composition (comprising the part of the puritied immunoglobulin or its epitope binding fragment is composition or its epitope binding fragment is composition or its epitope binding the action in the composition or its epitope binding the composition or its epitope binding the antibody. The composition or its epitope binding the presence or anticopy, and a concert of the presence or anticopy, and a concert of the presence or its synovial sarcoma, testicular cancer, thymic carcinoma, thymoma, thyroid metastatic cancer, and uterine cancers (carcinoma of the cervix, and uterine cancers). The polypeptide is useful for treating various human cancers, and diseases that express KID3, e.g. leukemias, prostate, ovarian or pancreatic cancers. The present sequence represents the G1 heavy chain of the mu-anti-KID3 humanized monoclonal The invention relates to a substantially purified immunoglobulin

Sequence 468 AA;

Gaps 1; Length 468; 10; Indels 85.1%; Score 627.5; DB 9; 87.5%; Pred. No. 3.7e-50; ive 6; Mismatches 10; Matches 119; Conservative Query Match Best Local Similarity ò

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New substantially purified immunoglobulin polypeptide or its epitope-binding fragment, which specifically binds to KID3, useful for treating

Sequence 136 AA;

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121 TTYGYFDVWGQGTTVT 136
                                              121 YA-DÝFDYWGÓGTÍLT 135
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RESULT

ADZ81889 standard; protein; 136 AA

ADZ81889;

14-JUL-2005 (first entry)

Anti-laminin-5 gamma2 heavy chain SEQ ID 86.

Laminin, cancer; cytostatic; neoplasm; antibody engineering; diagnosis; antibody; heavy chain.

Mus sp. Synthetic.

WO2005040219-A1

06-MAY-2005

28-OCT-2004; 2004WO-DK000744

28-OCT-2003; 2003US-00695559. 29-OCT-2003; 2003WO-EP012012.

20-NOV-2003; 2003US-0523895P 29-AFR-2004; 2004US-0565096P 06-MAY-2004; 2004US-056865SP 13-MAY-2004; 2004US-0511656P

NORDISK AS (BIOS-) BIOSTRATUM INC OVON (OVON)

Tryggvason K, Mathiasen IS, Padkar SB, Tarabykina S, Salo S; Boutard A; .

WPI; 2005-355824/36.

New laminin-5 gamma2-binding peptide that competes with mAb 5D5, mAb 6C12, or cross-competes with both 5D5 and 6C12, useful for diagnosing 6C12, or cross-compercontracting, or preventing cancer.

Disclosure; SEQ ID NO 86; 338pp; English

The invention relates to a peptide that competes with mab 5D5, mab 6C12, or cross-competes with both 5D5 and 6C12 in specifically binding to at least a portion of domain III of the gamma2 chain of human laminin.5 (Ln-5 gamma2 DIII). Also included are a composition comprising an amount of the isolated peptide and a pharmaceutical carrier, an assay for assessing the genara2-associated peptide content of a composition (comprising and ministering the peptide to the composition and attention whether the peptide binds any gamma2-associated peptides in the composition), a method of reducing cancer progression in a patient and a method of treating cancer in a patient. The peptide is a monoclonal antibody, preferably a humanized antibody or a fully human antibody. It binds a protein that is secreted from human cancer cells and or compound that kills cancer cells and/or to a detection agent. The peptide, or both the peptide and the nucleic acid, and the composition are useful in the preparation of a medicament for the treatment of cancer. The peptides, nucleic acids, and the composition are useful in the preparation of a medicament for the treatment of cancer. The peptides, nucleic acids, and composition are useful in the preparation of a medicament sequence represents a Anti-laminin-5 gamma2 antibody heavy chain. ADZ81889

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AACZ8

XXX
ADZ8

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ADZ8

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ADZ8

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XXX
ADZ8

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The invention relates to an antibody or its fragment, capable of extracellular region of a polypeptide encoded by a p53 apoptosis effector related to PMP-22 (PERD) gene. The invention also relates to a hybridoma that produces the antibody, a DNA encoding the antibody, a recombinant vector comprising the DNA, a host cell obtained by transducing the vector to the host cell, a method of producing the antibody and a therapeutic of the host cell, a method of producing the antibody and a therapeutic useful in an immunosessy for measuring the polypeptide encoded by the PERP gene, in the cell. The immunosessy is immunoprecipitation. The antibody is useful for measuring the expression of a polypeptide encoded antibody is useful as a reagent for detecting the polypeptide encoded antibody is useful as a reagent for detecting the polypeptide encoded antibody is useful as a reagent for detecting the polypeptide encoded by the PERP gene and for diagnosing the disease associated with a

Novel antibody capable of binding to three-dimensional structure of extracellular region of polypeptide encoded by p53 apoptosis effector related to PMP-22 gene, useful for manufacturing diagnostic and therapeutic agent for cancer.

WPI; 2006-056844/06. N-PSDB; AEE98108 Claim 13; SEQ ID NO 12; 121pp; Japanese

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                                                                           61 GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNOFFLOLNSVTSEDTATYYCARWDYG 120
                                                                                     61 GNRLEWMGYITYSGGTNYNPSLKSRISFTRDTSKNOFFLOLNSVTTEDTATYYCANNFYG 120
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                                                                                                                                                                                                                                                               Antibody therapy, diagnosis, p53 apoptosis effector related to PMP-22, PERP; cancer; neoplasm; cytostatic; immunotherapy.
                                     1 MRVLILLWLFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFP
                                                  1 MRVLILLWLFTAFPGILSDVHLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFP
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 Length 136;
                   Indels
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 DB 9;
84.5%; Score 622.5; DB 9;
86.0%; Pred. No. 2.7e-50;
ive 8; Mismatches 8;
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Ohta S, Hosaka E, Sasaki Y;
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                                                                                                                                                                                                                                             Murine PERP related protein #1.
                                                                                                                  136
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121 ---NFFDYWGQGTTLT 133
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                                                                                                                                                                                                                                                                                                                                                                         07-JUN-2004; 2004JP-00168116
                                                                                                                                                                                                                          (first entry)
                                                                                                                121 TTYGYFDVWGQGTTVT
          Best Local Similarity 86.0
Matches 117; Conservative
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                                                                                                                                                                                                                                                                                              Mus musculus
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 Query Match
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polypeptide encoded by the PERP gene. The disease is cancer. The antibody is useful in diagnoshing a disease by detecting or measuring the amount of a polypeptide encoded by the PERP gene in a cell, for treating cancer, for manufacturing a diagnostic, for detecting cancer and for manufacturing a therapeutic agent for cancer. This sequence represents a marine BERP related protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MRVLILLWLFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFP
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                                                                                                                                                                                                                                                                                                                                                                               Length 130;
                                                                                                                                                                                                                                                                                                                                                                            ; Score 593.5; DB 10; Length; Pred. No. 1.3e-47; 10; Mismatches 6; Indels
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                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49. .54
/label= CDR 1
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/label= CDR 2
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/label= CDR 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TTYGYFDVWGQGTTVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------WGQGTSVT 127
                                                                                                                                                                                                                                                                                                                                                                     query match 80.5%;
Best Local Similarity 81.6%;
Matches 111; Conservative 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95WO-JP002714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-333946/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT40804
                                                                                                                                                                                                                                                                                                                     Sequence 130 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       musculus
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Monoclonal antibodies which inhibit type II phospholipase A2 are useful in the treatment of myocardial infarction, cerebral infarction, acute kidney failure, chronic rheumatism, cardiac shock, pancreatitis, adult respiratory distress syndrome and colitis. The antibodies were generated by immunising Balb/C mice with recombinant human type II phospholipase A2. Spleen cells from the mice were fused with mouse myeloma P3U1 (P3x63Ag8.U1) and the hybridomas obtained were screened for phospholipase A2 inhibitory activity. Active clones were isolated including 12H5, 1.4 and 10.1. These were cultured and the antibody isolated from the culture supernatant by precipitation with ammonium sulphate and purification on a column of protein A Sepharose CLAB. Because the antibody acts on the primate and mouse forms of enzyme as well as human it is particularly suitable for preclinical testing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CNKLEWMGYISYSGFISYNPSLRSRISFTRDISKNOFFLOLNSVISEDTATYYCAR---- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GNKLERMGYIRYSGYISYNPSLKSRIFITRDTSQNQFFLHLTSVTTEDTATYYCTRDLDA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents the monoclonal antibody 1.4 heavy chain against type II phospholipase A2, from the present invention. The present invention describes a novel method for the amelioration of kidney
                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amelioration of kidney disorders caused by cisplatin administration - by treatment with an antibody inhibiting type II phospholipase A2 activity.
                                                                                                                                                                                                                                                                                                                                                                                          1 MRVLILLWLFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFP
                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRVLILLWLFTAFPGFLSDVQLQESGPGLVKPSQSLSLTCMVTGYSITSDYAWNWIRQFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal antibody, type II phospholipase A2; inhibition, cisplatin; amelioration; kidney disorder; nephrotoxicity; anticancer.
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody 1.4 heavy chain against type II phospholipase A2.
                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                   Length 136;
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                               79.9%; Score 588.5; DB 2
81.4%; Pred. No. 4.1e-47;
ive 4; Mismatches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 38; 74pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW44169 standard; protein; 136 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 WDYGTTYGYFDVWGQGTTVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 W-----YFDVWGAGTTVT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (YAMA ) YAMANOUCHI PHARM CO LTD.
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                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 81.4
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takasaki J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
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                                                                                                                                                                                                                                                                              Sequence 136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9749427-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW44169;
                                                                                                                                                                                                                                                                                                                   Query Match
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disorders (such as acute renal failure) associated with the
administration of cisplatin for the treatment of cancer. The method
comprises treatment with a monoclonal antibody which inhibits the
activity of type II phospholipase A2 (particularly of type II
possessing the same inhibitory activity and containing a part of the
antibody sequence. Preferably the antibody also inhibits the activity of
appearance in phospholipase A2, and has the ability to release
type II phospholipase A2, and has the ability to release
type II phospholipase A2, and has the ability to release
type II phospholipase A2, bound to a cell membrane. Three specific
monoclonal antibodies having these properties which can be used are 12H5,
10.1 and 1.4, derived from hybridomas FERM BP-5300, FERM BP-5298 and FERM
BP-5297 respectively. The method can be used for suppressing the
nephrotoxicity which is a characteristic feature of cisplatin
administration, and therefore allowing more efficient use of this drug as
an anticancer agent, e.g. by allowing an increased dosage to be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCAR---- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
heavy chain; variable region; mouse; monoclonal; hybridoma; PM1; plasmid;
pPM-k1; pPM-h1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRVLILLWLFTAFPGFLSDVQLQESGPGLVKPSQSLSLTCMVTGYSITSDYAWNWIRQFP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRVLILLWLFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.9%; Score 588.5; DB 2; Length 136; Best Local Similarity 81.4%; Pred. No. 4.1e-47; Matches 114; Conservative 4; Mismatches 11; Indels 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .18 //waiiilers //note= "Signal peptide" | 19. .137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19. .137
/note= "Mature peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR28671 standard; protein; 137 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 WDYGTTYGYFDVWGQGTTVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W-----YFDVWGAGTTVT 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92WO-JP000544
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pPM-h1 protein product
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N-PSDB; AAQ30756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 136 AA;
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30-MAR-1993
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                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                          9
                                                                                  The sequences given in AAR28670-71 were encoded by plasmids which were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma PMI which contained the plasmids pPM-k3 and pPM-h1. (Updated on 25-MAR-2003 to correct PN field.)
            human interleukin-6 receptor - has low V-region complementarily determining
                                                                                                                                                                                                                                                                               1 MRVLILLWLFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFP
                                                                                                                                                                                                                                                                                             2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Epidermal growth factor receptor; EGFR; tumourigenic; cytostatic; monoclonal antibody; mAb 806; antibody therapy; tumour.
                                                                                                                                                                                                                          Length 137;
                                                                                                                                                                                                                         Query Match 79.8%; Score 588; DB 2; Length 13
Best Local Similarity 83.8%; Pred. No. 4.6e-47;
Matches 114; Conservative 8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody 806 variable heavy chain (VH) region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "mAb 806 VH region"
                                                                 Disclosure; Page 122-123; 207pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .. .18
/note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB82796 standard; protein; 134 AA
            Reconstituted human antibody to antigenicity and contains mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                         136
                                                                                                                                                                                                                                                                                                                                                                                                           121 TT--AMDYWGQGTSVT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAY-2001; 2001US-0290410P.
28-SEP-2001; 2001US-0326019P.
21-DEC-2001; 2001US-0342258P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAY-2002; 2002WO-US015185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        121 TTYGYFDVWGQGTTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-129282/12.
N-PSDB; ABZ23940.
                                                                                                                                                                                                   Sequence 137 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200292771-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB82796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nice EC;
                                     regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
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12-MAR-2004; 2004WO-JP003334. 13-MAR-2003; 2003JP-00067832.

WO2004081048-A1

23-SEP-2004.

(CHUS) CHUGAI SEIYAKU KK

Fsuchiya M, Hirata Y; WPI; 2004-677525/66

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The invention relates to an isolated specific binding member (I) which recognizes an epidermal growth factor receptor (EGFR) epitope which is found in tumouriganic, hyperproliferative or abnormal cells and not detectable in normal cells. The EGFR epitope is located within the region comprising residues 273-501 of EGFR and does not demonstrate any amino acted sequence alterations or substitutions from normal EGFR. (I) is capable of binding the de2-7 EGFR at an epitope distinct from the bearrant expression, or in the absence of amplification of normal wild-type gene. The binding member comprises the VH and VL compyreptide sequence of monoclonal antibody (mAb) 806. (I) is useful for treating or diagnosing human or animal body, especially for treating tumour in a human. (I) is useful for the preparation of a medicament and to preventing or treating cancer which is located in or adjacent the brain, in a mammal. (I) is also useful for detecting the presence of amplified EGFR, de2-7EGFR or EGFR with high mannose glycosylation, where the brain, in a mammal. (I) is also useful for detecting that allow binding of the EGFR to the antibody to occur, and detecting that allow binding of the EGFR to the antibody to occur, and detecting whether binding has occurred between the EGFR from the sample and the antibody, where the detection of binding indicates that presence or activity of the EGFR in the mement of a tumour or cancer in the mammal. A pharmaceutical composition comprising (I), and optionally webicle, carrier or diluent is useful for detecting cancer in mammals, especially for treating brain-resident cancer in the mammal, accomposition comprising (I) and optionally webicle, especially for treating brain-resident cancers that produce aberrantly expressed EGFR in mammals, such as glioblastoma, medulloblastoma, meningioma, neoplastic ancers that produce aberrantly sypressed EGFR in earth to mammals. The present espresents the mammals constructions in mammals. The present espresents the preparent in mammals constructions 
                           Novel specific binding members, particularly antibodies recognizing epidermal growth factor receptor epitope found only in tumorigenic cuseful for diagnosing, preventing and treating cancer in mammals.
                                                                                                                                            6; Fig 14B; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               region
                                                                                                                                                Claim
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61 GNKLEWMGYISYSGNTRYNPSLKSRISITRDTSKNQPFLQLNSVTIEDTATYYCVTAGRG 120 GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYG 120 1 MRVLILLMEFTAFPGVLSDVQLQESGPSLVKPSQSLSLTCTVTGYSITSDFAMNWIRQFP 1 MRVLILLWLFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFP ς. . DB 6; Length 134; Score 586.5; DB 6; Length Pred. No. 6.2e-47; 4; Mismatches 14; Indels 121 TTYGYFDVWGQGTTVT 136 79.68; 83.18; ----FPYWGÖĞTLVT 131 Best Local Similarity 83.1 Matches 113; Conservative Sequence 134 AA; Query Match Best Local g g ò ò 용 8

9 9

Gaps

ADS14282 standard; protein; 255 ADS14282

Aurine protein relating to the invention SEQ ID NO:8. 16-DEC-2004 (first entry) ADS14282;

variant receptor; antidiabetic; haemostatic; endocrine; thrombocytopenia; type II diabetes; laron syndrome; thrombopoietin.

Mus musculus

having agonist activity with respect to a variant receptor. A ligard of the invention has antidiabetic, haemostatic, and endocrine-gen, activity. The ligand is useful for treating the disease caused due to variant receptor, which involves combining the disease caused due to variant receptor, where the disease is congenital non-megakaryocyte thrombocytopenia. A ligand of the invention is useful for transmitting a signal to a variant receptor which involves combining the variant receptor with the ligand of the invention is useful for treating diseases resulting due to variation receptor, such as type II diabetes and laron syndrome. The ligand enables signal transduction function of thrombopotetin, with respect to variant receptor. The present sequence is used in the exemplification of the invention. 61 GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYG 120 61 GNKLEWMGYITYSGYSIYNPSLKSRISISRDTSKNQLFLQLNSVTTEDTATYYCV---- 115 9 9 Novel ligand having agonist activity with respect to variant receptor e.g., variant thrombopoietin receptor, useful for treating disease resulting due to variant receptor such as congenital non-megakaryocyte 1 MRVLILLWLFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFP 1 MRVLIPLWLFTAFPGTLSDVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWSWIRQLP Gaps The invention relates to a novel ligand (preferably an antibody) (I) Score 569.5; DB 8; Length 255; Pred. No. 5e-45; 9; Mismatches 14; Indels 5; Example 4; SEQ ID NO 8; 132pp; Japanese. 121 TTYGYFDVWGQGTTVT 136 77.3%; Local Similarity N-PSDB; ADS14281. Sequence 255 AA; Query Match Matches g ò 셤 ò

Murine protein relating to the invention SEQ ID NO:14. ADS14288 standard; protein; 519 AA. 116 GGYDNMDYWGQGTSVT 131 (first entry) 16-DEC-2004 ADS14288; g

variant receptor; antidiabetic; haemostatic; endocrine; thrombocytopenia; type II diabetes; laron syndrome; thrombopoietin.

402004081048-A1 Mus musculus.

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                 having agonist activity with respect to a variant receptor. A ligand of the invention has antidiabetic, haemostatic, and endocrine-gen. activity. The ligand is useful for treating the disease caused due to variant receptor, which involves combining the ligand/antibody with the variant receptor, where the disease is congenital non-megakaryocyte thrombocytopenia. A ligand of the invention is useful for transmitting a signal to a variant receptor which involves combining the variant receptor with the ligand. The invention is useful for transmitting a resulting due to variation receptor, such as type II diabetes and laron syndrome. The ligand enables signal transduction function of thrombopoietin, with respect to variant receptor. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                              Novel ligand having agonist activity with respect to variant receptor e.g., variant thrombopoietin receptor, useful for treating disease resulting due to variant receptor such as congenital non-megakaryocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRVLIPLWLFTAFPGTLSDVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWSWIRQLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRVLILLWLFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFP
                                                                                                                                                                                                                                                      invention relates to a novel ligand (preferably an antibody) (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Consensus sequence of variable heavy chain region of anti-C3-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody; anti-C3-2; C3; C3a; C5a; complement activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 569.5; DB 8;
Pred. No. 1.1e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.3%; Sco...
79.4%; Pred. No. 1....
9; Mismatches
                                                                                                                                                                                                                           Disclosure; SEQ ID NO 14; 132pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammatory disease; kappa light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADO44274 standard; protein; 120 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TTYGYFDVWGQGTTVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGYDNMDYWGQGTSVT 131
                          12-MAR-2004; 2004WO-JP003334
                                                  13-MAR-2003; 2003JP-00067832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-OCT-2003; 2003WO-EP010989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-2004 (first entry)
                                                                           (CHUS ) CHUGAI SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 108; Conservative
                                                                                                    Tsuchiya M, Hirata Y;
                                                                                                                           WPI; 2004-677525/66
N-PSDB; ADS14287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                       thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 519 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004031240-A1
23-SEP-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADO44274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DVQLQESGPGLVKPSQSLSLTCTVAGYSITSDYAWNWIRQFPGNKLEWMGYISYSGSTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 NPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYGTTYGYFDVWGQGTTVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCAR-DYDGAYWYFDVWGAGTTVT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFPGNKLEWMGYISYSGFTSY
                                                                                                                                                                                                                        New molecule capable of inhibiting complement activation, and which specifically binds on a functional domain exposed on native human C3. useful for preventing or treating inflammatory diseases mediated by activation of complement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of variable heavy chain region of the anti-C3-2 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody; anti-C3-2; C3; C3a; C5a; complement activation;
inflammatory disease; kappa light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 556.5; DB 8
Pred. No. 3.5e-44;
3; Mismatches 9
                                                             (INNO-) INNOGENETICS NV.
(SANQ-) SANQUIN BLOOD SUPPLY FOUND AMSTERDAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SANQUIN BLOOD SUPPLY FOUND AMSTERDAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADO44271 standard; protein; 120 AA
                                                                                                                                                                                                                                                                                                                                          Example 12; Fig 17; 72pp; English.
                                                                                                                                     Hack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.5%;
04-OCT-2002; 2002EP-00447190.
16-OCT-2002; 2002US-0418947P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-OCT-2003; 2003WO-EP010989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-2002; 2002EP-00447190.
16-OCT-2002; 2002US-0418947P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105; Conservative
                                                                                                                                     Buysse M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Buysse M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INNO-) INNOGENETICS NV
                                                                                                                                                                                WPI; 2004-316465/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004031240-A1.
                                                                                                                                  De Winter H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Winter H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-APR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO44271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SANQ-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus sp.
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The specification describes a monoclonal antibody, designated anti-C3-2, which specifically binds on a functional domain exposed on native human C3, thus inhibiting the generation of the biologically active peptides such as C3a and C5a. The functional domain is in part located on the 23 kD-a-chain fragment of C3c. The antibody is useful for the preparation of a medicament for inhibiting complement activation, preferably for preventing or treating inflammatory diseases mediated by activation of complement. The present sequence represents the heavy chain region of the monoclonal antibody anti-C3-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DVQLQESGPGLVKPSQSLSLTCTVAGYSITSDYAWNWIRQFPGNKLEWMGXISYSGSTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inaulin-like growth factor-1 receptor, IGF-1R, tyrosine kinase activity, or epidermal growth factor receptor; EGFR, signal transduction pathway; ligand, tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NPSLRSRISFTRDTSKNOFFLQLNSVTSEDTATYYCARWDYGTTYGYFDVWGQGTTVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFPGNKLEWMGYISYSGFTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                             New molecule capable of inhibiting complement activation, and which specifically binds on a functional domain exposed on native human C3. useful for preventing or treating inflammatory diseases mediated by
                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                75.5%; Score 556.5; DB 8; Length 120; 89.0%; Pred. No. 3.5e-44; ive 3; Mismatches 9; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antipsoriatic; antibody;
                                                                                                                                                  Disclosure; Fig 14B; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ76886 standard; protein; 127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leger O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-IGF-1R related protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JAN-2003; 2003WO-FR000178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                   activation of complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corvaia N,
               WPI; 2004-316465/29.
N-PSDB; ADO44270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-569653/53
                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                  Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003059951-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                  105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goetsch L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADJ76886;
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                    Best Local
Matches 10
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fragments, that bind to human insulin-like growth factor-1 receptor (IGF-1R) and optionally: (i) inhibit natural binding of insulin-like growth factor-1 receptor (IGF-1R) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-1R. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-1R and/or spidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YISYDGTNNYKPSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCAR--YGRV--FFDY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; immunoglobulin; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                    68
                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LLTAIPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YISYSGFTSYNPSLRSRISFTRDTSKNOFFLQLNSVTSEDTATYYCARWDYGTTYGYFDV
                                                                                                                                                                                                                                                                                                                                                                                                                    9 LFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFPGNKLEWMG
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                     4.
                                                                                                                                                                                                                                                                                                                                                 Length 127;
                                                                                                                                                                                                                                                                           protein sequence used to generate the Ab of the invention
                                                                                                                                                                                                                                                                                                                                              Score 554; DB 7; Length 12
Pred. No. 6.5e-44;
6; Mismatches 13; Indels
Disclosure; SEQ ID NO 52; 164pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "leader peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADZ67056 standard; protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61. .76
/note= "CDR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "CDR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "CDR1"
                                                                                                                                                                                                                                                                                                                                               75.2%;
82.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-DEC-2003; 2003US-00735916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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/note= "~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .116
                                                                                                                                                                                                                                                                                                                                                                al Similarity 82.0
105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WGQGTTVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WGOGTTLT 124
                                                                                                                                                                                                                                                                                                               Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS2005084906-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129
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                                                                                                                                                                                                                                                                                                                                                                                     Matches
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 %XCCCCCCCCCCCCCCX%
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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a ctivation of the IGF-IR and/or EGFR, and/or of EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin treceptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent and/or IERZ/neudependent cells into the contract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (1), which is optionally labeled. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, breast cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or for the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the prevention of a medicament contended for the prevention of a medicament cancer and the specific targeting of a biologically active compound to intended for the specific targeting of a biologically active compound to its useful for in vitro diagnosis of illnesses induced by an
                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for preparation of a medicament intended to inhibit the growth and/or the proliferation of tumor cells, preferably 1GF-dependent, especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is useful in the preparation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s with (I), which is optionally labeled. The present in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 8; SEQ ID NO 52; 125pp; English.
  2002FR-00000653
                        [8-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753
2014A-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for treating cancer.
                                                                                                                                                                                                                                                                                                         Corvaia N,
                                                                                                                                                                                                                                                                                                                                                     2005-321968/33
                                                                                                                                      GOETSCH L.
CORVAIA N.
LEGER O.
                                                                                                                                                                                                     DUFLOS A.
                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADZ67055
                                                                                                                                                                                                                                                             BECK A.
18-JAN-2002;
18-JAN-2002;
07-MAY-2002;
                                                                                                                                                                                                                                                                                                         Goetsch L,
                                                                                                                                                                                                                                  (HAEU/)
(BECK/)
                                                                                                                                        (GOET/)
                                                                                                                                                                 CORV/)
                                                                                                                                                                                      LEGE/)
                                                                                                                                                                                                          (DUFL/)
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Matches 105; Conservative Best Local Similarity σ Query Match

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YISYSGFTSYNPSLRSRISFTRDTSKNOFFLOLNSVTSEDTATYYCARWDYGTTYGYFDV 128 LFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFPGNKLEWMG 68 Gaps 4. 75.2%; Score 554; DB 9; Length 127; 82.0%; Pred. No. 6.5e-44; ive 6; Mismatches 13; Indels Sequence 127 AA; 69

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antibody; insulin; tumor suppressor; cytostatic; pharmaceutical; breast tumor; endocrine disease; gynecology and obstetrics, neoplasm; prostate tumor; andrology; genitourinary disease; colorectal tumor; gastrointestinal disease; lung tumor; respiratory disease; bladder tumor; eraal tumor; thyroid tumor; osteosarcoma; musculoskeletal disease; pancreas tumor; multiple myeloma; hematological disease; monoclonal antibody.
61 YISYDGTNNYKPSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCAR--YGRV--FFDY 116
                                                                                                                                                                                                                                                                                                                                                                                                                             Beck A;
                                                                                                                                                  Murine monoclonal antibody 7C10 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                           Duflos A, Haeuw J, Leger O,
                                                                                       AEE61302 standard; protein; 127 AA
                                                                                                                                                                                                                                                                                                                                                                                                         (FABR ) FABRE MEDICAMENT SA PIERRE
                                                                                                                                                                                                                                                                                                                                                       2002FR-00005753.
2003WO-FR000178.
2003FR-00008538.
                                                                                                                                                                                                                                                                                                                16-DEC-2004; 2004US-00012353
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                                                                                                                                                                                                                                                                                                                                               2002FR-00000654
                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             Goetsch L, Corvaia N,
                    WGQGTTVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2005-784616/80.
N-PSDB; AEE61301.
                                      117 WGQGTTLT
                                                                                                                                                                                                                                                                         US2005249730-A1.
                                                                                                                                                                                                                                                     Mus musculus.
                                                                                                                                                                                                                                                                                                                                                        07-MAY-2002;
20-JAN-2003;
                                                                                                                                                                                                                                                                                                                                                                                      16-DEC-2003;
                                                                                                                                                                                                                                                                                                                                                                            11-JUL-2003;
                                                                                                                                                                                                                                                                                                                                     8-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                8-JAN-2002;
                                                                                                                              09-FEB-2006
                                                                                                                                                                                                                                                                                             10-NOV-2005.
                                                                                                          AEE61302;
                    129
                                                                   RESULT 1:
AEE61302
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Beck A;

Duflos A, Haeuw J,

Leger O,

The invention relates to a novel humanized anti-insulin like growth factor I receptor (IGF-IR) antibody (Ia), anti-insulin/IGF-5 hybrid receptor (IGF-IR) antibody (Ib), or anti-iGF-IR and hybrid-R antibody (Ic) or their antigen-binding fragments, comprising a complementary determining region of non-human origin and a framework region having a human residue, and capable of inhibiting in vivo tumor growth. A composition of the invention has cytostatic activity. An antibody of the invention is useful for determining regression progression or onset of a pathological disorder characterized by increased expression and/or activation of human IGF-IR, hybrid-R to both IGF-IR and hybrid-R relative to normal. A pharmaceutical composition of the invention is useful for the treatment or prevention of a disorder chosen from breast cancer, the treatment or prevention of a disorder chosen from breast cancer, colorectal cancer, blanded cancer, blanded cancer, colorectal cancer, backers and myebloma. The present sequence represents a heavy chain variable region isolated from monoclonal antibody 7C10.

New humanized anti-insulin like growth factor I receptor (IGF-IR) antibody, anti-insulin/IGF-5 hybrid receptor (hybrid-R) antibody, or anti-IGF-IR and hybrid-R antibody, for treating cancer.

Example 8; SEQ ID NO 52; 144pp; English

Sequence 127 AA;

Query Match

9; Length 127; DB 75.2%; Score 554;

Search completed: May 19, 2006, 17:40:02 Job time : 161.667 Becs

GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd. Copyright

protein - protein search, using sw model

May 19, 2006, 17:40:37 ; Search time 25.9048 Seconds Run on:

(without alignments) 505.138 Million cell updates/sec

US-09-889-936A-6

Perfect score:

1 MRVLILLWLFTAFPGILSDV.......WDYGTTYGYFDVWGQGTTVT 136 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:*
1: pir::*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

EX	Description	Ig heavy chain pre	Ig heavy chain pre	chain	neavy chain	neavy chain	neavy	neavy	leavy	neavy	neavy chain V	neavy chain V	neavy	neavy cha	nu chain pre	neavy chain V	neavy chain V	leavy	neavy	leavy	neavy chain V	neavy chain V	neavy	neavy	e C72-3A1 pr	heavy chai	heavy chain V	heavy	heavy cha	Ig variable region
SUMMAKIES	Ω	PL0100	B24672	S30752	AVMS35	HVMS1B	507637	HVMS31	538718	S37200	128195	C53285	T01262	E25114	D33932	F25114	C25114	A25114	HVMS73	S42771	859639	S14485	D25114	S26464	I57810	S26467	₹.	144	S13687	377
	80	~	7	7	-	ч	~	ч	~	~	N	N	N	~	~	~	~	~	н	7	~	~	~	N	N	~	Н	~	~	~
	Length	135	134	149	137	116	136	116	116	121	117	119	114	119	115	115	119	120	117	123	106	100	119	106	117	104	113	102	111	140
d	Query Match	:		78.6														65.7	64.7	63.6	63.2	63.0	62.8	62.8	62.6	61.8	61.2	59.9	59.3	59.3
	Score	605.5	587.5	579	561	557	555.5	539	525.5	524	522	509	508.5	504	498.5	494	487	484.5	476.5	469	466	464.5	463	462.5	461	455.5	451	441.5	437	437
		-	8	m	4	S	9	7	æ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23				27		29

Ig heavy chain V r	Ig heavy chain V r	heavy	heavy	_	heavy	heavy	heavy	-	Ig heavy chain V r	-	heavy	heavy	Ig heavy chain V r	heavy o	Ig heavy chain pre
S14484	S13685	S13686	S14487	S14486	S13688	831690	830530	831511	526461	S31586	831512	809711	S31676	S13519	878055
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0	7	N	8	•			•••	"	•	N	(A	~	7	7	N
101 2	112 2	112 2	102 2	102	110	130	123	155 2	94	•	••	••	•	147 2	145 2
									56.2 94	139	155	146	137		
59.2	29.0	58.6	58.0	57.9	57.8	9.95	56.4	56.4		55.8 139	55.6 155	55.1 146 ;	54.6 137	54.3	53.9

ALIGNMENTS

```
RESULT 1
```

PL0100
Ig heavy chain precursor V region (40-140) - mouse
C;Species: Mus musculus (house mouse)
C;Species: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999

C;Accession: PL0100
R;Near, R.I.; Haber, B.
MOI. Immunol. 26, 371-382, 1989
A;Titler Characterization of the heavy and light chain immunoglobulin variable region ger A;Titler number: PL0100; MUID:89238344; PMID:2497340
A;Accession: PL0100

A;Molecule type: DNA
A;Residues: 1-135 <NEA>
A;Residues: 1-135 <NEA>
A;Cross-references: UNIPARC:UPI0000114EA6; GB:M27660; NID:g341745; PIDN:AAA58746.1; PID:c
A;Experimental source: strain A/J
A;Experimental source: strain A/J
C;Genetics:

Ajutrons: 15/1 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-18/Domain: signal sequence #status predicted <SIG> F;19-115/Domain: W segment #status predicted <VRE> F;31-116/Domain: Immunoglobulin homology <IMD> F;31-116/Domain: D segment #status predicted <ARE> F;117-118/Domain: J segment #status predicted <ARE>

5; Gaps Length 135; Indels Query Match 82.2%; Score 605.5; DB 2; Best Local Similarity 82.4%; Pred. No. 2.6e-45; Matches 112; Conservative 12; Mismatches 7;

1;

9 1 MRVLILLWLFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFP g ò

116 61 GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYG 120 61 GNRLEWMGYITYNGYTTYNPSLKSRFSITRDTSKNQLFLQLSSVTTEDTATYYCAR---g ઠે

121 TTYGYFDVWGQGTTVT 136 ŝ

117 -SYDYFDYWGQGTTLT 131

g

RESULT 2
B24672
Cj Abeavy chain precursor V region (VGAM3-2) - mouse
Cj Species: Mus musculus (house mouse)
Cj Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 18-Oct-1996
Cj Accession: B24672
RjWinter, E.; Radbruch, A.; Krawinkel, U.
RjWinter, E.; Radbruch, A.; Krawinkel, U.
A; Riminter, E.; Radbruch, A.; Krawinkel, U.
A; Reference number: A91022; MUID:86055722; PMID:2998759

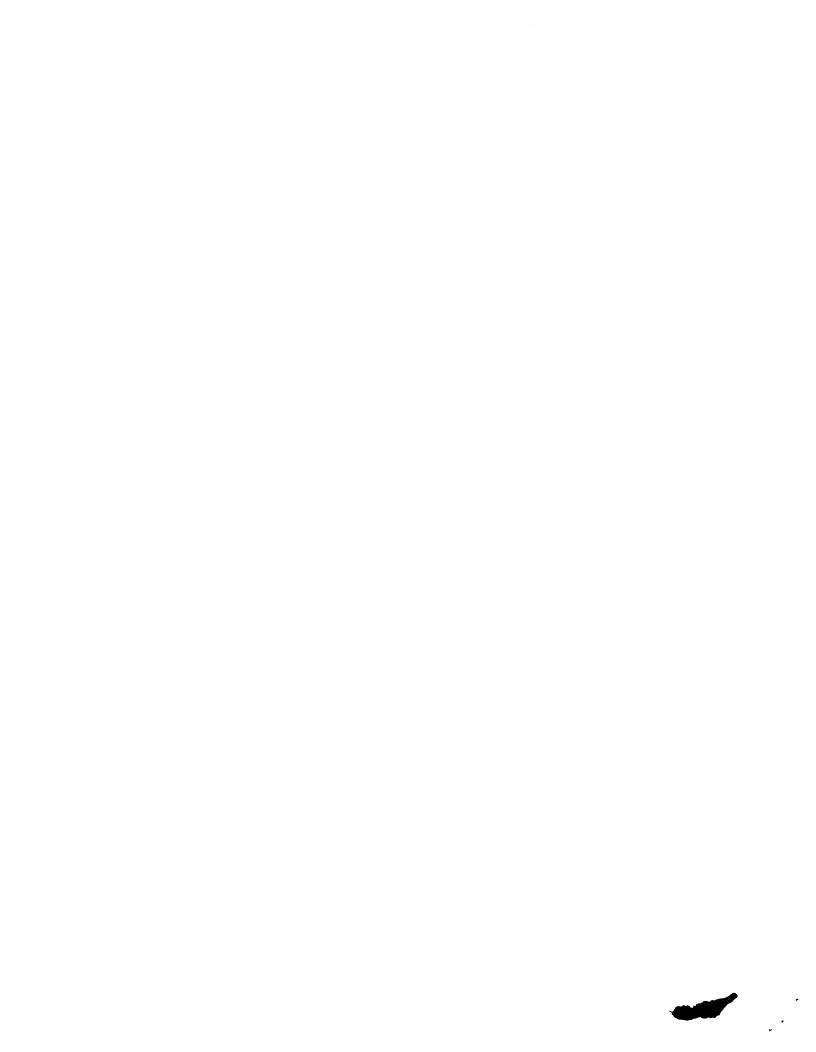
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Matches 106; Conservative
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Cispecies: Misculus (house)
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A Molecule type: DNA
A, Residues: 1-134 <WIN>
A, Cross-references: UNIPARC: UPI00001768F5
A, Cross-references: UNIPARC: UPI00001768F5
C, Genetics:
A, Introns: 15/1
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heterotetramer; immunoglobulin
F;19-134/Product: Ig heavy chain V region VGAM3-2 #status predicted
F;33-116/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 83.1%; Pred. No. 9e-44
Matches 113; Conservative 7; Mismatches
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A; Title: Cloning, sequencing and expression of the rearranged MOPC 315 VH gene segment. A; Reference number: PL0102; MUID:89238351; PMID:2497341
A; Accession: PL0102
A; Molecule type: mRNA
A; Residues: 1-137 < RIN>
A; Residues: 1-137 < RIN>
A; Residues: 1-137 < RIN>
A; Residues: UNIPROT: P01822; UNIPARC: UP1000002727B; GB:M27638; NID:g602706; PIDN:FA; Rishinental source: strain MOPC 315
B; Rinfited to the BMBL Data Library, June 1988
A; Reference number: S03262
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A, Molecule type: protein
A, Molecule type: protein
A, Molecule type: protein
A, Residues: 1, Xr. 3-11, Xr. 14-21 < SCH>
A, Cross references: UNIPARC: UP1000017373F
A, Cross references: UNIPARC: UP1000017378F
A, Note: the authors translated mRNA in vitro to obtain the precursor protein
B, Francis, S.H.; Leslie, R.G.Q.; Hood, L.; Eisen, H.N.
Proc. Natl. Acad. Sci. U.S.A. 71, 1123-1127, 1974
A, Title: Amino-acid sequence of the variable region of the heavy (alpha) chain of a mouse
A, Reference number: A93787; MUID: 74170779; PMID: 4524622
A, Molecule type: protein
A, Residues: 19-52, Kr. 53-75, BVGB, 80-101, 'D', 103-106, 'ZB', 109-122, 124-137 < FRA>
A, Cross-references: UNIPARC: UP10000173740, R.
A, Cross-references: UNIPARC: UP10000173740, R.
A, Cross-references: NA948B, Padlan, E.A., Davies, D.R., Pecht, I., Givol, D., and Wrigh
A, Reference number: A948B, M. Givol, D.; Ricca, G.A.
MOL: Immunol. 29, 21-30, 1992
A, Title: Cloning and expression of the variable regions of mouse myeloma protein MOPC315
A, February and expression of the variable regions of mouse myeloma protein MoPC315
A, February and expression of the Variable regions of mouse myeloma protein MoPC315
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A;Molecule type: DNA
A;Redesidues: 1-15,'G(,16-137 <RI2>
A;Coss-references: UNIPARC:UPI000016CE1C; EMBL:X07880; NID:g51760; PIDN:CAA30727.1; PID:
B;Jilka, R.L.; Pestka, S.
Proc. Natl. Acad. Sci. U.S.A. 74, 5692-5696, 1977
A;Title: Amino acid sequence of the precursor region of MOPC-315 mouse immunoglobulin her
A;Reference number: A93814; MUID:78094475; PMID:414225
A;Accession: A93814
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A;Rosidues: 19-137 <CHES-
A;Cross-references: UPIDNPARC:UPIO000113794; EMBL:X63972; NID:953532; PIDN:CAA45384.1; PID:
C;Comment: This alpha chain was isolated from a myeloma protein that has anti-dinitropher
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C;Reywords: heterotetramer; immunoglobulin
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-136/Product: Ig heavy chain V region (MOPC 315) #status experimental <MAT>
F;33-116/Domain: immunoglobulin homology <IMM>
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A, Residues: 1-14, H', 16-31 cJL>
A, Residues: 1-14, H', 16-31 cJL>
A; Cross-references: UNIPARC: UDI000017373E
A; Note: the authors translated mRNA in vitro to obtain the precursor protein
R; Schechter, I.; Wolf, O.; Zemell, R.; Burstein, Y.
Fed. Proc. 38, 1839-1845, 1979
A; Title: Structure and function of immunoglobulin genes and precursors.
A; Reference number: A91462; MUID: 79148758; PMID: 428562
A; Accession: A91462
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C;Accession: J0509
R;Levy, N.S.; Malpiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary in A;Reference number: JT0501; MUID:89279149; PMID:2499654
A;Accession: JT0509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: S38718
                                                                                                                                                                                                                                                                       Ig heavy chain precursor V region (M315) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKVLSLLYLLTAIPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYMWIRQFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DVQLQESGPGLVKPSQSLSLTCAVTGYSITSDYAWNWIRQFPGNKLEWMGYISYSGTTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCAR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-116 <LEV>
A; Residues: 1-116 <LEV>
A; Cross-references: UNIPROT: P18531; UNIPARC: UPI00000278E0
A; Experimental source: strain BALB/cJ
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-116/Product: Ig heavy chain V region (MN15) #status predicted <MAT>
F;33-116/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tch 73.1%; Score 539; DB 1; al Similarity 87.1%; Pred. No. 1.2e-39; 101; Conservative 7; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 525.5; DB 2
Pred. No. 1.7e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R'Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
A;Reference number: $38713
A;Accession: $38718
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                                121 TTYGYFDVWGQGTTVT 136
                                                                                                 118 DGYHFFTYWGÓGTLVT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: translation not shown
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Best Local Similarity
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Cispeciaes Mus musculus (house mouse)
Cispeciaes Mus musculus (house mouse)
Cispeciaes Mus musculus (house mouse)
Ciscossion: 807637
Riuakov, D.N.; Deev, S.M.; Polyanovsky, O.L.
Riuchev, D.N.; Deev, S.M.; Polyanovsky, O.L.
A; Reference number: 807637; MUD: 90067954; PMID: 2587273
A; Reference number: 807637; MUD: 90067954; PMID: 2587273
A; Residues: 1-136 <URA>
A; Residues: 1-136 <URA
A; Residues: 1-13
                                                                                                                                                                                                                                   Ig heavy chain precursor V region (1843) - mouse (5/Species: Mus musculus (house mouse) (5/Species: Mus musculus (house mouse) (5/Accession: 1950 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004 (5/Accession: JT0508 W.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J. A; Exp. Malipiero, D.V.; Lebecque, S.G.; Gearhart, P.J. A; Ext. Malipiero, D.C. Somatic mutation in immunoglobulin VH genes during the primary A; Reference number: JT0501; MuID:89279149; PMID:2499654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MRVLILLWLFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFP 60
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A;Residues: 1-116 cLEV>
A;Cross-references: UNIPROT:P18532; UNIPARC:UPI00000278E1
A;Cross-references: UNIPROT:P18532; UNIPARC:UPI00000278E1
A;Rover: this sequence belongs to the VH3660 subfamily
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Superfamily: immunoglobulin V region; immunoglobulin
F;1-18/Domain: signal sequence #status predicted cSIG>
F;19-116/Product: Ig heavy chain V region (1B43) #status predicted cMAT>
F;33-116/Domain: immunoglobulin homology cIMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-116/Domain: immunoglobulin homology <IMM>
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Pred. No. 5.2e-41;
9; Mismatches 18; Indels
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121 TTYGYFDVWGQGTTVT 136
                                                                120 HLY-YFDYWGQGTTLT 134
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Best Local Similarity 77.9%;
Matches 106; Conservative
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A,Title: Molecular characterization of monoclonal anti-steroid antibodies: primary struct and their pH-reactivity profiles
A,Feference number: A33285; MUID:92017897; PMID:1922102
A,Accession: C52285
A,Status: preliminary
A,Molecule type: MRNA; protein
A,Residues: 1-119 <SAW>
A,Cross-references: UNIPARC:UPIO00011D0A5; GB:D12734; NID:9220548; PIDN:BAA02226.1; PID: S,Note: sequence extracted from NCBI backbone (NCBIN:63297, NCBIP:63302)
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-119 <OLL>
A;Cross-references: UNIPARC:UP10000115D24; GB:X01378; NID:952007; PIDN:CAA27095.1; PID:91
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
C;Accession: T01262
R;Pirofski, L.A.; Thomas, E.K.; Scharff, M.D.
R;Pirofski, L.A.; Thomas, E.K.; Scharff, M.D.
A;Tibles: Hum. Retroviruses 9, 41-49, 1993
A;Title: Variable region gene utilization and mutation in a group of neutralizing murine A;Reference number: Z14288; MUID:315.2585; PMID:7678971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region (HP25) - mouse
C,Species: Mus musculus (house mouse)
C,Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Accession: E25114
R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
EMBO J. 4, 3681-3688, 1985
A;Title: The idiotypic network and the internal image: possible regulation of the internal image. Possible regulation of the internal image. Possible regulation of the internal image.
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                                                                                                                                                                                                                                                                                                                                                                            Score 509; DB 2;
Pred. No. 4.6e-37;
8; Mismatches 11;
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Pred. No. 4.8e-37;
6; Mismatches 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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82.2%;
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Best Local Similarity 80.7%;
Matches 96; Conservative
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97; Conservative
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A; Residues: 1-117 < SHE>
A; Residues: 1-117 < SHE>
A; Residues: 1-117 < SHE>
A; Cross-references: UNIPPAC: UPI0000114D72; GB:M19775; NID:g195526; PIDN:AAA38343.1; PID: A; Note: the authors translated the codon AAC for residue 61 as Thr, and did not translat C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C'Species: Mus musculus (house mouse)
C'Date: 01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C'Date: 101-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C'Accession: 128195
R'Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A;Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid A;Reference number: A28195; MUID:88153717; PMID:3267217
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                                                                                                                                                                                                                                                                                         A;Molecule type: mRNĀ
A;Residues: 1-121 <FIS.>
A;Residues: 1-121 <FIS.>
A;Cross-references: UNIPARC:UPI00001161AC; EMBL:X74587; NID:g402639; PID:g402640
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <INM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NPSLKNRISITRDTSKNQPFLKLNSVTTEDTATYYCAR---GGIYGYDDYFDSWGGGTTL 117
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     Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus rusculus (house mouse)
C;Bate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C;Accession: S37200
R;Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F. submitted to the EMBL Data Library, August 1993
A;Description: Production and cloning of TMV-specific monoclonal antibodies. A;Reference number: S37200
A;Reference number: S37200
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 524; DB 2;
Pred. No. 2.4e-38;
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85.6%; Pred. No. 3.4e-38;
iive 5; Mismatches 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.1%;
82.6%;
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Matches 100; Conservative
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A;Molecule type: mRNA
A;Residues: 1-115 <01Lb.
A;Cross-rences: UNIPARC:UPI0000115D28; GB:X03379; NID:g52013; PIDN:CAA27101.1; PID:g
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IVM>
                                                                                                                                                                                                                                                                                                                                                                                                                            Ig mu chain precursor V region (E7) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 23-May-1997
C;Accession: D3392
R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-1A,Reference number: A33932; MUID:89282823; PMID:2499887
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                                                                                                                                                                    DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFPGNKLEWMGYISYSGFTSY
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                                                                pry Match 68.4%; Score 504; DB 2; Length 119;
st Local Similarity 81.5%; Pred. No. 1.2e-36;
tches 97; Conservative 5; Mismatches 13; Indels
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Pred. No. 8.6e-36;
8; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-115 <BAC.
A;Croses-references: UNIPARC:UPI00001768F1; GB:M27106
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;33-115/Domain: immunoglobulin homology <IMM>
/ords: heterotetramer; immunoglobulin
98/Domain: immunoglobulin homology <IMM>
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79.1%;
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Matches 97; Conserv
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Best Local Similarity
Matches 91; Conserv
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A; Status: preliminary
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us-09-889-936a-6.rup

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GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd.
                   Copyright
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ON votein - protein search, using sw model

May 19, 2006, 17:34:57; Search time 207.238 Seconds (without alignments) 607.041 Million cell updates/sec Run on:

US-09-889-936A-6 737

Title: Perfect score:

1 MRVLILLWLFTAFPGILSDV......WDYGTTYGYFDVWGQGTTVT 136

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

2849598 segs, 925015592 residues Searched:

2849598 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q5u41	Q99m22 mus	P01822 mus musculu				Q569b8 rattus norv				Q53vr3 mus	Q53vr7 mus				Q53vr2 mus				E Q65zil mus musculu			Omot 7xm2 Domo	Q6gmx1 homo	Ogenical Oge		rattu	Q5i0l9 rattus norv			,
	ID	Q5U413 MOUSE	Q99M22 MOUSE	HV46 MOUSE	Q569B6 RAT	HV61 MOUSE	Q6LBQS MOUS	Q569B8_RAT	HV60 MOUSE	Q53VQ5 MOUSE	O53VQ1_MOUS	Q53VR3_MOUSE	Q53VR7 MOUSE	HV62 MOUSE	Q53VQ4 MOUS	Q53VQ9_MOUSE	Q53VR2_MOUSE	Q53VR6_MOUSE	Q53VQ0_MOUSE	HV47 MOUSE	Q65ZI1 MOUSE	Q53VQ8 MOUS	1			Q6GMX6 HUMAN	Q6P4I8 HUMAN	QSIOJ1_RAT	QSIOL9_RAT	HV43 MOUSE	Q6NYH3 HUMAN	E . C . C
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ouery	Match	82.7	77.1	76.1	76.1	75.6	75.4	74.4	73.1	68.4	67.0	66.1	65.7	64.7	64.2	'n.	62.7	ď.	ä	61.2	61.1	60.1	58.1	57.5	57.0	٠.	54.2	۳.	ω.		ω.	,
	Score	609.5	568	561	561	557	555.5	548	539	504	494	487	484.5	476.5	473	463	462	458	453	451	450	443	428.5	423.5	420	403.5	399.5	397.5	395	392.5	392	
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Q9ul73 homo sapien P06331 homo sapien Q5m842 rattus norv Q72374 homo sapien Q86sx2 homo sapien Q96x8 homo sapien Q96x9 homo sapien Q95973 homo sapien Q95973 homo sapien Q91x92 mus musculu Q9tx4 homo sapien Q6mx5 homo sapien Q6gmx5 homo sapien Q6bul0 homo sapien
Q9UL73 HUMAN Q5M942 RAT Q72374 HUMAN Q96EX2 HUMAN Q96EX2 HUMAN Q96EX8 HUMAN Q96EX8 HUMAN Q96QB8 HUMAN Q91G9B8 HUMAN Q91G9B HUMAN Q91G9B HUMAN Q91G9B HUMAN Q91G HUMAN Q96GMX5 HUMAN Q96GMX5 HUMAN
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1119 1444 1492 1493 1493 1493 150 150 150 150 150 150 150 150 150 150
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
386.5 386.5 386.5 382.5 382.5 34.5 374.5 374.5 368 368 368
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# ALIGNMENTS

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STRAIN-FVB/N; TISSUE—Colon;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L.; Feingold E.A., Grouse L.H.; Derge J.G.,

A Rlausner R.D., Collins F.S., Magner L., Shenmen C.M.; Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Dokins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Distchench L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Radion M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. M. March D. M. Malaysis of more than 15,000 full-length human
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                            07-DEC-2004, integrated into UniProtKB/TrEMBL. 07-DEC-2004, sequence version 1. 07-FEB-2006, entry version 18.
                                                                            483 AA.
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Ensembl; ENSMUSG0000054328; Mus musculus.
                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR001599; Ig.
InterPro, IPR001110; Ig-11ke.
InterPro, IPR001597; Ig-c1.
InterPro, IPR001596; Ig-WHC.
InterPro, IPR001596; Ig-v.
                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                        LOC544903 protein.
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                                                                                                                                                                                                                                                                                                        Name=LOC544903
                                                                        QSU413_MOUSE
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                                MOUSE
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Distributed under the Creative Commons
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P01822;
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                                                                                                                                                                                                                                                                        1 MRVLILLWLFTAFPGILSDVQLQESGPDLVKPSQSLSLTCTVTGYSTTSGYGWHWIRQFP
                                                                                                                                                                                                                                                1 MRVLILLMLFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchoncoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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STRAIN-Mix FVB/N; TISSUE-Mammary tumor. WAP-TGF alpha model. 7 months
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                             3;
                                                                                                                                                                      82.7%; Score 609.5; DB 2; Length 483; 85.4%; Pred. No. 2.4e-50; ive 6; Mismatches 11; Indels 3;
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR013106; V-set.

SMART; SM00409; IG; 2.

SMART; SM00407; IG; 2.

SMART; SM0406; IGv; 1.

PROSITE; PSS0835; IG_LIKE; 4.

PROSITE; PS00290; IG MC; UNKNOWN 2.

SEQUENCE 483 AA; 52714 MW; 7CZ72DA501A4A0D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001, integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                  121 TTYGY-FDVWGQGTTVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                     119 GNYDYAMDYWGQGTSVT 135
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                                                                                                                                                                                            Best Local Similarity 85.4 Matches 117; Conservative
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Name=LOC238447;
                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                      Query Match
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MEDLINE-89238351; PubMed=2497341; DOI=10.1016/0161-5890(89)90133-8;
Rinfret A., Horne C., Dorrington K.J., Klein M.;
"Cloning, sequencing and expression of the rearranged MOPC 315 VH gene seqment.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRVLILLWLFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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Attribution-Noberivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.1%; Score 568; DB 2; Length 47 79.4%; Pred. No. 2.5e-46; cive 9; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        768E39A138918892 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
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MEDLINE=74170779; PubMed=4524622;
Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             roc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977)
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07-MAR-2006, entry version 51.
heavy chain V region MOPC 315 precursor.
Mus musculus (Mouse).
                                                                                HSSP; P01820; 1G7J.
Ensembl; ENSMUSG00000054328; Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
SEQUENCE 479 AA; 51992 MW; 768E3
                                                        EMBL; BC002091; AAH02091.1; -; mRNA
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                                                                                                                                   InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003509; IG.
InterPro; IPR003506; IG.
InterPro; IPR003506; IG.
InterPro; IPR003506; IG.
InterPro; IPR013106; V-Bet.
Pfam; PR07564; CI-8et; 2.
SMART; SM00409; IG; 2.
SMART; SM00409; IG; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GNKLEWLGFIKYDGSNGYNPSLKORVSITRDTSENQFFLKLNSVTTEDTATYYCA-GDND 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
"Arino-acid sequence of the variable region of the heavy (alpha) chain of a mouse myeloma protein with anti-hapten activity."; Pyco. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRVLILLMLFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFP
                                         "SEQUENCE REVISION TO 53.

MEDLINE=77244979; PubMed=268248;

Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;

Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;

"Model-building studies of antigen-binding sites: the hapten-binding site of mopc-315.";

Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).

-I- MISCELLANEOUS: This alpha chain was isolated from a myeloma protein that has anti-dinitrophenyl activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
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/FTId=PRO 0000015232.
Framework-1.
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G -> GG (in Ref. 1; CAA30727).

G -> H (in Ref. 2).

GY -> YG (in Ref. 4).

N -> D (in Ref. 4).

Missing (in Ref. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.1%; Score 561; DB 1; Length 137; 77.9%; Pred. No. 3e-46; Live 12; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Complementarity-determining-1.
Framework-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Complementarity-determining-3.
Framework-4.
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                                                                                                                                                                                                                                                                                                                          Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OSCUBE RAT PRELIMINARY; PRT; 615 AA. Q569B6; 10-MAY-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                    EMBL; M27638; AAA61337.1; -; Genomic_DNA.
EMBL; X07880; CAA30727.1; -; Genomic_DNA.
PIR; PL0102; AVMS35.
HSSP; P01820; 1G7.
SMR; P01820; 1G-137.
ENSEMBL; ENSWISGO0000057048; Mus musculus.
InterPro; IPR003599; 1g-1;
InterPro; IPR003100; Ig-1;
InterPro; IPR003100; Ig-1;
InterPro; IPR013106; V-set.
PROSITE; SM00409; IG; 1.
SMART; SM00409; IG; 1.
PROSITE; PSS0835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin dom
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Matches 106; Conservative
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NEDLINE=2218825; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Klausher R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,

A Botchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,

B Capleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Comnetein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Rotriguez A.C., Garimwood J., Schmutz J., Myers R.M.,

B Noting A. Schein J.B., Jones S.J.M., Marra M.A.;

R Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                            Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
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80.3%; Pred. No. 1.6e-45;
tive 8; Mismatches 17; Indels
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PROSITE; PS00290; IG MHC; UNKNOWN 3.
SEQUENCE 615 AA; 67986 MW; BE5C2483C69F186C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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10-MAY-2005, sequence version 1.
OYFEB-2006, entry version 12.
LOC314509 protein.
Name=LOC314509;
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InterPro; IPR00310; Ig-like.
InterPro; IPR00310; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003096; Ig_WHC.
InterPro; IPR013106; V-set.
Pfam; PR07654; Cl-set; 4.
SMART; SM00409; IG; 1.
SMART; SM00407; IGc1; 2.
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120 PLTGRYFDYWGOGVMVT 136
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Best Local Similarity 80.31
Matches 110; Conservative
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Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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PDB; 1KCS; X-ray; H=25-116.
BDB; 1KCV; X-ray; H=25-116.
BDB; 1KCV; X-ray; H=25-116.
BDB; 1KCV; X-ray; H=25-116.
BDB; 1KCV; Y-ray; H=25-116.
BDB; 1KCV; Y-ray; H=25-116.
InterPro; 1PR001310; Ig-like.
InterPro; 1PR013106; V-set; 1.
SMART; SN00406; IGV; 1.
SMART; SN00406; IGV; 1.
3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
SIGNAL
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                                                                                        01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
                                     116 AA.
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                                                                                                               01-NOV-1990, sequence version 1.
07-MAR-2006, entry version 44.
Ig beavy chain V region 1843 precursor.
Mus musculus (Mouse).
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                                  STANDARD;
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Matches 166; Conserv
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Distributed under the Creative Commons Attribution-NoDerivs License
                            1 MRVLILLCLFTAFPGILSDVQLQESGPDLVKPSQSLSLTCTVTGYSITSGYSWHWIRQFP
MRVLILLUMLFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFP
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                                                                                                       61 GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNOFFLOLNSVTSEDTATYYCAR 116
                                                                                                                                   61 GNKLEWMGYIHYSGNTSYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCAR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRVLILLWLFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90067954; PubMed=2587273;
Urakov D.N., Deev S.M., Polyanovsky O.L.;
"The extructure of the expressible VH gene from a hybridoma producing
monoclonal antibodies against porcine transferrin.";
Nucleic Acids Res. 17:9481-9481(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 75.4%; Score 555.5; DB 2; Length 136; Best Local Similarity 77.9%; Pred. No. 1e-45; Matches 106; Conservative 9; Mismatches 18; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 AA; 15307 MW; SB0F439CCFB15C3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 RAT

Q569B8_RAT PRELIMINARY; PRT; 590 AA.

Q569B8.

10-8AY-2005, integrated into UniProtKB/TrEMBL.

10-MAY-2005, sequence version 1.

07-FEB-2006, entry version 13.

RQD1359202 protein.
                                                                                                                                                                                                                                                                                                                                             05-JUL-2004, integrated into UniProtKB/TrEMBL. 05-JUL-2004, sequence version 1. 05-BB-2006, entry version 11. VH gene product (Fragment).
                                                                                                                                                                                                                                                                                             136 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X16740; CAA34714.1; -; Genomic_DNA. HSSP; P18532; 1XCV. SNR; QE18532; 1Z0-136. Ensembl; ENSMUSGG0000057048; Mus musculus.
                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003100; Ig-like.
InterPro; IPR013106; V-Set.
SWART; SW00409; IG; 1.
PR051TE; PS50835; IG LIKE; 1.
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                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                        QELBQS MOUSE
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Q569B8 RA
ID Q569
AC Q569
DT 10-M
DT 07-F
DE RGD1
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116 AA.

PRT;

STANDARD;

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HV60 MOUSE
                       P18531;
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                                                                                                                                   MEDLINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDLINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Riausner R.D., Colling F.S., Wagner L., Shammen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heishe F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Maray D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Abramson M. Macken M.C., Stanchez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Macken M.A., Schnetch A., Schein J.B., Jones B.J.M., Marra M.A., Schein J.B., Jones B.J.M., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                   Ratus norvegicus (Rat).
B.karyota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Wysmmalia, Buthoria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 74.4%; Score 548; DB 2; Length 590; Best Local Similarity 78.4%; Pred. No. 2.7e-44; Matches 105; Conservative 11; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, BC092580; AAH92580.1; -; mRNA.
InterPro; IPR003599; Ig-
InterPro; IPR003599; Ig-
InterPro; IPR003597; Ig-11.
InterPro; IPR003597; Ig-21.
InterPro; IPR003596; Ig-V.
InterPro; IPR00409; Ig-V.
SWART; SW00409; IG-1.
SWART; SW00409; IG-1.
PROSITE; PS00299; IG-IKE; S.
PROSITE; PS00299; IG-IKE; S.
PROSITE; PS00299; IG-IKHC; UNKXOWN 3.
PROSITE; PS00299; IG-IKHC; UNKXOWN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
TISSUE=Spleen;
NIH MGC Project;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.
                                                                                                                         NUCLEOTIDE SEQUENCE
                                                                                       NCBI_TaxID=10116;
   Name=RGD1359202;
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RESULT 8 HV60_MOUSE

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                                                                                                                                                                                                                                         Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
"Early onset of somatic mutation in immunoglobulin VH genes during the
                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                   PDB; 1EZV; X-ray; X=20-116.
Ensembl; ENSWUSG0000057048; Mus musculus.
Enterbro; IPR007110; Ig-like.
Interbro; IPR013106; V-set.
Interpro; IPR013106; V-set.
Pfam; PP07466; V-set.
SWART; SM04406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRVLILLWLFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GNKLEWMGYISYDGSNNYNPSLKNRISITRDTSKNQFFLKLNSVTTEDTATYYCAR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCAR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                       MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Framework-2. Complementarity-determining-2. Framework-3. By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V region M315.
/FTId=PRO_0000015241.
Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 73.1%; Score 539; DB 1; Length 11 Best Local Similarity 87.1%; Pred. No. 3.4e-44; Matches 101; Conservative 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13095 MW; 4562E03E53DC9E10 CRC64;
01-NOV-1990, integrated into UniProtKB/Swiss-Prot. 01-NOV-1990, sequence version 1. 07-NAR-2006, entry version 39. Ig heavy chain V region M315 precursor. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                           primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                      PIR; JT0509; HVMS31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 AA;
                                                                                                                                             NCBI_TaxID=10090;
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49
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Immunoglobulin domain.
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NON TER 115 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                    Fougereau M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q53VR3_MOUSE
                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
O43VR3_MOUSE
                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                MEDLINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
Ollier P. a germiline network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQFPGNKLEWMGYISYDGSHNY
                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFPGNKLEWMGYISYSGFTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Edkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Marmalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi, Murodea, Muridae, Murinae, Mus.
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NUCLEOTIDE SEQUENCE.
MEDLINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 504; DB 2; Length 119;
Pred. No. 8.5e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Indels
                                                                                                                                                                                                                                                                             Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 AA; 13931 MW; 502E51A5213F056E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAY-2005, integrated into UniProtKB/TrEMBL. 24-MAY-2005, sequence version 1. 07-FB2-2006, entry version 4. 07-FB2-2006, entry version 4. 1. region (Fragment).
                                                    24-MAY-2005, integrated into UniProtKB/TrEMBL, 24-MAY-2005, sequence version 1.
7-FBB-2006, entry version 4.
VH-D-JH region (Fragment).
                                119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 68.4%; Score 504; DB 1. Similarity 81.5%; Pred. No. 8.5e-97; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q53VQ1 MOUSE PRELIMINARY; PRT;
Q53VQ1;
                                PRT;
                                                                                                                                                                                                                                                                                                                                                 EMBL; X03378; CAA27095.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR001109; Ig.
Interpro; IPR007110; Ig-like.
Interpro; IPR007110; Ig-like.
Interpro; IPR007109; Ig-v.
SWART; SW00409; IG, 1.
SWART; SW00406; IGV; I.
Immunoglobulin domain.
NON_TER
                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE OF 28-29.
                               PRELIMINARY;
                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               SMR; Q53VQ5; 1-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                 NCBI_TaxID=10090;
                              Q53VQ5_MOUSE
Q53VQ5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON TER
SEQUENCE
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G53VQ1 MOUSE
D53VQ1 MC
AC G53VQ1 M
DT 24-MAY-20
DT 24-MAY-20
DT 24-MAY-20
DT 24-MAY-20
DF VH-D-JH
OS IN WH-D-JH
OC EVKaryot
OC EVKaryot
OC Mawmalia
OC MAWIOJGGA
OX NCBI
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Distributed under the Creative Commons Attribution-NoDerivs License
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"The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAI system.";
EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DVQLQESGPGLVKPSQSLSLTCSVTGYSIISGYYWNWIRQFPGDKLEWMGFIRYDGSNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFPGNKLEWMGYISYSGFTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 NPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYGTTYGYFDVWGQGT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NPSLKTRISITRDTSKNQPFLRLNSVTTEDTATYYCAVFGYDMDYYAMDYWGQGT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                             Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases
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115 115
115 AA; 13257 MW; D465A5854DF459A3 CRC64;
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79.1%; Pred. No. 7.6e-40;
iive 8; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-2005, integrated into UniProtKB/TrEMBL. 24-MAY-2005, sequence version 1. 77-EBS-2006, entry version 4. VH-D-JH region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X03376; CAA27083.1; -; mRNA.
SMR; Q53VR3; 1-19.
InterPro; IPR003599; IG.
InterPro; IPR003596; IG-like.
InterPro; IPR003596; IG-v.
SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X03379; CAA27101.1; -; mRNA.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                               NUCLEOTIDE SEQUENCE OF 28-29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 79.1
nes 91; Conservative
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NCBI_TaxID=10090;
                                                                                                                             MOUSE
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 NPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARW-----DYGTTYGYFDVWGQGT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NPSLKNRISITRDISKNQFFLKLNSVTTEDJATYYCARPLYFRHDEEYYDVMDYWGQGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                        DVQLQESGPGLVKPSQSLSLTCSVTGNSITSGYY#SWIRQPPGNKLEWMGYIKYDGNNSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                              79 NPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDY----GTTYGYFDVWGQGT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DVHLQESGPGLVKPSQSLSLTCSVTGYSITRGYNWNWIRRFPGNKLEWMGYINYDGSNNY
                                                                                                                                                                                                                                                                                                                   19 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFPGNKLEWMGYISYSGFTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                           Gaps
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Pred. No. 6.7e-39;
8; Mismatches 16; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
MEDLINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
"The idiotypic network and the internal image: possible regul
                                                                                                                                                                                         Length 119;
                                                                                                                                                                                                                                                    16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                             119 AA; 13799 MW; 36504D1665BFBB59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 AA; 13892 MW; 013452306EBAA3BE CRC64;
                                                                                                                                                                                      Score 487; DB 2;
Pred. No. 3.8e-39;
5; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAY-2005, integrated into UniProtKB/TrEMBL. 24-MAY-2005, sequence version 1. 07-FBB-2006, entry version 4. Mus musculus (Fragment).
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EMBL; X03374; CAA27071.1; -; mRNA.
SMR; Q53VR7; 1-120.
InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin domain.
NON_TER
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PROSITE; PSS0835; IG_LIKE; 1.
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NUCLEOTIDE SEQUENCE OF 28-29.
                                                                                                                                                                                      ch 66.1%;
1 Similarity 79.0%;
94; Conservative
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Q53VR7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBO J. 4:3681-3688(1985).
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                                                                                            119
                             Immunoglobulin domain.
NGN TER
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Best Local Similarity
Matches 91; Conserv
                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                       SEQUENCE
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1 MRVLILLWLFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSG-YAWNWIRQF 59
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                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BALB/cJ;
MEDLINES 82279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
"Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.";
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                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ĵ. Exp. Med. 169:2007-2019(1989).
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 64.7%; Score 476.5; DB 1; Length 117; Best Local Similarity 75.2%; Pred. No. 3.9e-38; Matches 88; Conservative 15; Mismatches 13; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain V region 733./Frid=PRO_000015243.
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                                                         01-NOV-1990, integrated into UniProtKB/Swiss-Prot
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053V04.
053V04.
24-MAY-2005, integrated into UniProtKB/TrEMBL.
24-MAY-2005, sequence version 1.
07-FEB-2006, entry version 3.
VH region (Fragment).
Mus musculus (Mouse).
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By similarity.
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SMR; P18533; 19-117.
Ensembl; ENSMUSG0000059520; Mus musculus.
                                                                                           01-NOV-1990, sequence version 1.
07-MAR-2006, entry version 37.
Ig heavy chain V region 733 precursor.
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InterPro; IPR003596; Ig v.
InterPro; IPR013106; V-8et.
Pfam; PF07686; V-8et; I.
SMART; SM00406; IGv; I.
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STANDARD;
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Query Match
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Dictributed under the Creative Commons Attribution-NoDerivs License
[1]
NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
NUCLEOTIDE 86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
Ollier P., Rocca-Serra dit the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
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24-MXY-2005, sequence version 1.
07-FEB-2006, entry version 4.
WH-D-UH region (Fragment).
Mus musculus (Mouse)
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Euarchontoglires; Glires; Rodentia, Sciurognathi;
Muroidea, Muridae, Murinae, Mus.
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tive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                     Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
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Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 NPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCAR 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X03378; CAA27096.1; -; mRNA.
SMR; OS3VQ4; 1-98.
Ensembl; ENSMISGO0000557048; Mus musculus.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PR05ITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 473;
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SMR; Q53VQ9; 1-118.
InterPro; IPR003599; IG.
InterPro; IPR007110; IG-11ke.
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NUCLEOTIDE SEQUENCE OF 28-29.
                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE OF 28-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.28;
                                                                                                                                                                                                EMBO J. 4:3681-3688 (1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 89.8
Matches 88; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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053 VO9 MOU
DD 724-MA
DT 24-MA
DT 24-M
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DR InterPro; IPR001596; Ig_v.
DR SMART; SM00406; IG_v.
DR SMART; SM00406; IG_v.
DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin domain.
FT NON_TER 119 119
SQ SEQUENCE 119 AA, 13844 MW; 6B1BC8C7DC77E147 CRC64;

Cuery Match

Conservative 10; Mismatches 16; Indels 4; Gaps

Matches 88; Conservative 10; Mismatches 16; Indels 4; Gaps

Oy 19 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYWSWFRQFPGDKLEWMGYISYSGFTSY 78

DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYWSWFRQFPGDKLEWMGYISYSGFTSY 78

DVQLQESGPGLVKPSQSLSLTCSVTGYSIASGYYWSWFRQFPGDKLEWMGYISYSGFTSY 78

OY 79 NPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCAR---WDYGTTYGY-FDVWGQG 132

OY 79 NPSLRSRISFTRDTSKNQFFLQLNSVTPEDTATYYCAR---WDYGTTYGY-FDVWGQG 132

DD 61 NPSLKNRISITRDTSKNQFFLRLNSVTPEDTATYFCVRPLXYRFDBEXYYATDYWGQG 118
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Search completed: May 19, 2006, 17:46:30 Job time : 209.238 secs

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                                                                May 19, 2006, 17:46:56 ; Search time 39.3968 Seconds (without alignments) 302.161 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13,
                                                                                                                           1 MRVLILLWLFTAFPGILSDV......wDYGTTYGYFDVWGQGTTVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11
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                                                                                                                                                                                                                                                                                    Issued Patents AA:*
1. /BMC Celerra SIDS3/ptodata/2/iaa/5_COMB.pep:*
2. /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3. /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4. /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5. /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
5. /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7. /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7. /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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        GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-436-717-31
US-08-767-128-18
US-08-308-494A13
US-08-913-555-11
US-08-913-555-11
US-08-211-980-23
US-08-211-980-23
US-08-211-980-23
US-08-211-980-23
US-08-466-163B-7
US-09-802-096-7
US-09-925-179-7
US-09-925-179-7
US-09-940-725B-2
US-09-940-727B-13
US-09-940-727B-13
US-09-200-105-207C-2
US-09-200-105-207C-2
US-09-200-105-207C-2
US-09-200-105-207C-2
US-09-200-105-207C-2
US-09-200-105-207C-2
US-09-200-105-207C-2
                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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                                                                                                                                                                            650591 segs, 87530628 residues
                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               protein search, using sw model
                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                         US-09-889-936A-6
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Match Length DB
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                                     om protein - F
                                                                                                                                                                             Searched:
                                                                                                                              Seguence:
                                                                                                                                                                                                                                                                                      Database
                                                                   Run on:
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No.
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27 500 67.8 130 2 US-09-802-096-5 Sequence 5, Appli 29 500 67.8 130 2 US-09-802-075-5 Sequence 5, Appli 30 500 67.8 130 2 US-09-802-075-5 Sequence 5, Appli 30 500 67.8 134 2 US-08-466-151-3 Sequence 3, Appli 31 500 67.8 134 2 US-08-466-163-3 Sequence 3, Appli 33 500 67.8 134 2 US-09-802-077-3 Sequence 3, Appli 34 500 67.8 134 2 US-09-802-077-3 Sequence 3, Appli 34 500 67.8 134 2 US-09-802-077-3 Sequence 3, Appli 36 65.5 213 2 US-09-802-077-3 Sequence 3, Appli 36 65.5 213 2 US-09-802-107-1058-2 Sequence 13, Appli 37 482.5 65.5 241 2 US-09-902-107-1058-2 Sequence 13, Appli 39 482.5 65.5 496 2 US-08-902-486-15 Sequence 13, Appli 473 64.2 117 1 US-08-672-345C-10 Sequence 10, Appli 47 473 64.2 117 1 US-08-672-345C-10 Sequence 10, Appli 47 473 64.2 117 1 US-08-672-345C-10 Sequence 10, Appli 48 473 64.2 117 2 US-09-214-095D-11 Sequence 10, Appli 49 473 64.2 117 2 US-09-214-095D-11 Sequence 10, Appli 49 473 64.2 117 2 US-09-512-345C-10 Sequence 10, Appli 49 473 64.2 117 2 US-09-512-345C-10 Sequence 10, Appli 49 473 64.2 117 2 US-09-514-095D-11 Sequence 10, Appli 49 473 64.2 117 2 US-09-514-095D-11 Sequence 10, Appli 40 MPJ 473 64.2 117 2 US-09-514-095D-11 Sequence 10, Appli 40 MPJ 473 64.2 117 2 US-09-514-095D-11 Sequence 10, Appli 40 MPJ 473 64.2 117 2 US-09-514-095D-11 Sequence 10, Appli 40 MPJ 473 64.2 117 2 US-09-514-095D-11 Sequence 10, Appli 40 MPJ 473 64.2 117 2 US-09-514-095D-11 Sequence 10, Appli 40 MPJ 413 64.2 117 2 US-09-514-095D-11 Sequence 10, Appli 41 473 64.2 117 2 US-09-514-095D-11 Sequence 10, Appli 41 473 64.2 117 2 US-09-514-095D-11 Sequence 10, Appli 41 473 64.2 117 2 US-09-514-095D-11 Sequence 10, Appli 41 473 64.2 117 2 US-09-514-095D-11 Sequence 10, Appli 41 473 64.2 117 2 US-09-514-095D-11 Sequence 10, Appli 41 473 64.2 117 2 US-09-514-095D-11 Sequence 10, Appli 41 473 64.2 117 2 US-09-514-095D-11 Sequence 10, Appli 41 473 64.2 117 2 US-09-514-095D-11 Sequence 10, Appli 41 473 64.2 117 2 US-09-514-095D-11 Sequence 10, Appli 41 473 64.2 117 2 US-09-514-095D-11 Sequence 10, Appli 41 473 64.2 117
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### ALIGNMENTS

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NESULT 1

US-08-137-1170-31

US-08-137-1170-31

SQUENEAL 13. Application US/08137117D

PRECENT No. 5795505

GENERAL INFORMATION:
APPLICANT: SATO, KOh
APPLICANT: BENDIG, MAY
APPLICANT: BENDIG, MAY
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCES 158
CORRESPONDENCES 158
COUNTRY: USA
ZIP: 20007-5109
COUNTRY: USA
ZIP: 20007-5109
COUNTRY: IBM PC COMPALIABLE
COUNTRY: IBM PC COMPALIABLE
COMPUTER READABLE FORM:
MEDIUM TYPER: PLOREY disk
COMPUTER: IBM PC COMPALIABLE
COMPATING DATE: 24-ARR-1992
PRICE APPLICATION NUMBER: WO PCT/JP92/O0544
FILING DATE: 19-FEB-1992
PRICE PRICE APPLICATION NUMBER: S9466/126/AAOK
TELEPHONE: (202)672-5399
FELENCOMMULATION NUMBER: S9466/126/AAOK
TELEPHONE: (202)672-5399
TELEPHONE: (202)672-5399
TELEPHONE: HARDAR ECHARAPERISTICS
TELEPHONE: LANGER HARDICS
TEL
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61 GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYG 120
                                                                                                                                                                                                                                                                                                                                                          61 GNKLEWMGYISYSGITTYNPSLKSRISITRDISKNQFFLQLNSVTTGDTSTYYCARSLAR 120
                                                                                                                                                                                                                       1 MRVLILLWLFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFP 60
                                                                                                                                                                                                                                                      1 MRVLILLMLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh St
CITY: Minneapolis
STATE: MN
                                                                                                                      Length 137;
                                                                                                                   79.8%; Score 588; DB 1; Length 13' 83.8%; Pred. No. 1.1e-49; tive 8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18, Application US/08767128
Fatent No. 6111079
GENERAL INFORMATION:
APPLICANT: WILLE, DWANE E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: GOBEE, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
NUMBERS OF SEQUENCES: 46
CORRESPONDENCE: MACCHAIR, Gould, Smith, Edell, Welter & STREET: 3100 No. 6111079west Center, 90 South Seven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIPICATION 19434

PRIOR APPLICATION DATA
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION NUMBER: 08/41,373
FILING DATE: 05-JUN-1995
PRIOR APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: CATTER: Charles G.
REGISTRATION NUMBER: 35,093
REFERRACE/DOCKET NUMBER: 35,093
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              121 TTYGYFDVWGQGTTVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TT--AMDYWGOGTSVT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                        Query Match 79.8
Best Local Similarity 83.8
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                     TOPOLOGY: linear; MOLECULE TYPE: protein US-08-436-717-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  612/332-9081
amino acid
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                                                                                                                                                                                                                                                                                                                                                          61 GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLAR 120
                                                                                                                                                                                                                         1 MRVLILLWLFTAFPGILSDVQLQESGFGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFP 60
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                          5;
                                                                                                                   Score 588; DB 1; Length 137;
Pred. No. 1.1e-49;
8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 31, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: BENDIG, Mary
APPLICANT: DENDIG, Mary
APPLICANT: DENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: SALDANHA, JOSE
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY & LATGMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILING DATE:
CLASSIFICATION NUMBER: US/08/430,/1/
PILING DATE:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRION APPLICATION NUMBER: UP 4-32084
FILING DATE: 19-FEB-1992
PRION APPLICATION NUMBER: UP 3-95476
FILING DATE: 25-APR-1991
APPLICATION NUMBER: UP 3-95476
FILING DATE: 25-APR-1991
ATORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 25-ABR-1991
ATORNEY/AGENT INFORMATION:
ATORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 25-258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELEBONMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
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TT---AMDYWGQGTSVT 134
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INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                              TTYGYFDVWGQGTTVT 136
                                                                                                                   Query Match
Best Local Similarity 83.8%;
Matches 114; Conservative
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                                          MOLECULE TYPE: protein
TYPE: amino acid
TOPOLOGY: linear
                                                       ; MOLECULE TYP!
US-08-137-117D-31
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US-08-913-555-11
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NPSLKSRISITRDTSKNOPFLQLNSVTTEDTATYYCAR--CGNYPWYFDYWGQGTTLT 116
                                                                                                                                                                                                                                                                                                                                                                                                                   79 NPSLRSRISFTRDISKNOFFLOLNSVISEDIATYYCARWDYGTTYGYFDVWGQGTTVT 136
                                                                                                                                                                                                                                                                                                                            19 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFPGNKLEWMGYISYSGFTSY
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                      Query Match 73.4%; Score 541; DB 2; Length 119; Best Local Similarity 87.3%; Pred. No. 3.4e-45; Matches 103; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/08308494A
Patent No. 5959083
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Tetravalent Bispecific Receptors, The
TITLE OF SEQUENCES: 24
CORRESPONDENCE: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIOO5-3315
COMPUTER: IBP PC COMPATIBLE
COMPUTER: IBP PC COMPATIBLE
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENTINO NUMBER: US/08/308,494A
FILING DATE: 21-SEP-1994
CLASSIFICATION NUMBER: US 07/891,739
FILING DATE: 01-JUN-1992
CLASSIFICATION NUMBER: DE P4118120.4
FILING DATE: 03-UNN-1991
ATTORNEY GATEN INFORMATION:
NAME: Kulik, David J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 05552-1186-02000
TELECOMMONICATION NUMBER: 05552-1186-02000
TELECOMMONICATION INFORMATION:
TELEEDHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 117 amino acids
amino acid
                                                                                                                                                   internal
                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                             ANTI-SENSE: NO FRAGMENT TYPE: 1 ORIGINAL SOURCE: US-08-767-128-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-08-308-494A-13
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1 LQESGPDLVKPSQSLSLTCTVTGYSITSGYSWHWIRQFPGNKLEWMGY1QYSGITNYNPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 PSLRSRISFIRDTSKNQFFLQLNSVISEDTATYYCARWDY-GTTYGYFDVWGQGTTVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PSLKNRISITRDTSKNQFFLKLNSVTTEDTATYYCAVYYDGSS---FDYWGQGTTVT 115
                                                                                                       22 LQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFPGNKLEWMGYISYSGFTSYNPS
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                                                                                                                                                                                                          82 LRSRISFTRDISKNQFFLQLNSVTSEDTATYYCARWDYGTTYGYFDVWGQGTTVT 136
                                                                                                                                                                                                                                    1;
       Length 117;
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                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: SEINO, Ken-ichiro
APPLICANT: KAYGAKI, No. 6068841uhiko
APPLICANT: YAGITA, Hideo
APPLICANT: VAGITA, Hideo
APPLICANT: OKUMURA, Ko
APPLICANT: NAKATA, Motomi
TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
NUMBER OF SOUGHNES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCDERMOCL, WILL & EMERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,059
FILING DATE:
71.3%; Score 525.5; DB 1;
85.2%; Pred. No. 1.1e-43;
tive 7; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: McDermott, Will & Emery STREET: 99 Canal Center Plaza CITY: Alexandria STATE: Virginia COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/09065059 Patent No. 6068841
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TELEPHONE: 703-518-5100
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BUCCA Ph.D., Daniel
REGISTRATION NUMBER: P-42.
REFERENCE/DOCKET NUMBER: 2
  Query Match
Best Local Similarity 85.23
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide US-09-065-059-11
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                                                                   APPLICANT: KAYAGAKI, No. 6946255uhiko
APPLICANT: YAGITA, Kideo
APPLICANT: YAGITA, Kideo
APPLICANT: YAGITA, Kideo
APPLICANT: NCHMORA, Ko
APPLICANT: NCHMORA, KO
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY
TITLE OF INVENTION: REACTING WITH FAS LIGAND AND PRODUCTION PROCESS THEREOF
NUMBER OF SEQUENCES:
ADDRESSEE: MCDERMOLT, Will & EMETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQPPGNKLEWMGYISYDGSNNYN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 VOLOESGPGLVKPSOSLSLTCSVTGYSITSGYAWNWIROFPGNKLEWMGYISYSGFTSYN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PSLKARISITRDISKAQPFLKLASVITEDTATYYCAVYYDGSS---FDYWGGGTTVT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDY-GTTYGYFDVWGQGTTVT 136
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US-08-111-080-23
is Sequence 23, Application 08/111080
is Sequence 23, Application 08/111080
is Sequence 23, Application 08/111080
is GENERAL INFORMATION:
APPLICANT: O'DINO, TRUNGYA
in TITLE OF INVENTION: HIV Immunotherapeutics
in CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
is STRET: 6300 Sears Tower, 233 S. Wacker Drive
is CITY: Chicago
is STATE: 111inois
is COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vergion #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,555
FILING DATE: 19-SEP-1997
CLASSIFICATION: S10
ATTORNEY/AGENT INFORMATION:
NAME: BLOCCH PLD., Daniel
REGISTRATION NUMBER: 42,368
REFERENCE/DOCKET NUMBER: 50356-150
TELECOMONICATION INFORMATION:
TELECOMONICATION INFORMATION:
TELECOMONICATION INFORMATION:
                                                                                                                                                                                                                                     STREET: 99 Canal Center Plaza, Suite 300 CITY: Alexandria STATE: Virginia
Sequence 11, Application US/08913555
Patent No. 6946255
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-756-8699
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-913-555-11
                                                                                                                                                                                                                                                                                                                                                       Virginia
: USA
                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
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79 NPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYGTTYGYFDVWGQGTTVT 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFPGNKLEWMGYISYSGFTSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23, Application US/08211980
Patent No. 566559
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/111,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: USA
                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 92
FILING DATE: 22-AUG-1991
FILING DATE: 22-AUG-1991
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
FILING DATE: 24-AUG-1992
APPLICATION NUMBER: 0S 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REGISTRATION NUMBER: 25,447
REGISTRATION NUMBER: 31629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION: 424
CIASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6408
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.1;
Matches 98; Conservative
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amino acid
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 NPSLRSRISFTRDTSKNOFFLQLNSVTSEDTATYYCARWDYGTTYGYFDVWGQGTTVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NPSLKSRISITRDTSKNLFFLQLSSVTSEDTATYYCAR------GSFGDWGQGTLVT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 69.3%; Score 510.5; DB 1; Length 114; Best Local Similarity 83.1%; Pred. No. 3e-42; Matches 98; Conservative 5; Mismatches 8; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23, Application PC/TUS9307967
; Sequence 23, Application PC/TUS9307967
; GENREAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORESPONDENCES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: 111inois
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07967
                   APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AEBNT INFORMATION:
NAME: BOTUN, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELEFONMUNICATION INPORMATION:
TELEFONDE: (312) 474-6500
TELEFAX: (312) 474-648
TELEFAX: (312) 474-048
TELEFAX: (312) 474-048
TELEFAX: S5-3856
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24 AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22 APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 314
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SO ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (312) 474-6300
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-211-980-23
                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90909
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19 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFPGNKLEWMGYISYSGFTSY 78
                                                                                                                                                                                                                           1 EVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISYSGSTTY 60
                                                                                                                                                                                                                                                                                                 79 NPSLRSRISFIRDTSKNOFFLQLNSVTSEDTATYYCARWDYGTTYGYFDVWGQGTTVT 136
                                                                                                                                                                                                                                                                                                                           61 NPSLKSRISITRDISKNLFFLQLSSVTSEDIATYYCAR-----GSFGDWGQGTLVT 111
                                                                                                                                                7; Gaps
                                                                                          Score 510.5; DB 5; Length 114;
Pred. No. 3e-42;
5; Mismatches 8; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 137;
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Pred. No. 4.6e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2C1D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
RIGHT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION NUMBER: 07/879495
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08466151
Patent No. 6037453
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81.0%;
                                                                                               Query Match
Best Local Similarity 83.1%;
Matches 98; Conservative
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TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US93-07967-23
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APPLICANT: Dresta, Leonard G.
TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
FILE REFERENCE: P0718P2C2US
CURRENT FILING DATE: 2001-03-08
CURRENT FILING DATE: 2001-03-08
PRIOR PPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: PCT/US92/06860
PRIOR FILING DATE: 1992-06-07
PRIOR FILING DATE: 1992-06-07
PRIOR FILING DATE: 1992-06-07
PRIOR FILING DATE: 1992-06-07
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
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81.0%; Pred. No. 4.6e-42;
iive 7; Mismatches 13;
                                                                                                                                                                                                                                                                Query Match 69.1%; Score 509.5; DB 2; Best Local Similarity 81.0%; Pred. No. 4.6e-42; Matches 98; Conservative 7; Mismatches 13;
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; LENGTH: 137
  PCT/US92/06860
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98; Conservative
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Matches 9
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APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
APPLICANT: Presta, Leonard G.
APPLICANT: Presta, Leonard G.
APPLICANT: Presta, Leonard G.
APPLICANTON WUMBER: US/09/802,096
ACURRENT APPLICATION WUMBER: US/09/802,096
ACURRENT FILING DATE: 2001-03-08
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1994-01-26
                                                                                                                                              61 NPSLKRRISITRDTSKNQFFLQLNSVTTEDTATYYCARGSIYYYGSRYRYFDVWGAGTTV 120
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                                            19 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFPGNKLEWMGYISYSGFTSY
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    13; Indels
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Best Local Similarity 81.0%; Pred. No. 4.6e-42;
Matches 98; Conservative 7; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-16
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR PILING DATE: 1992-05-07
    7; Mismatches
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Patent No. 6685939
    98; Conservative
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SEQ ID NO 7
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; ORGANISM: Mus musculus
US-08-466-1638-7
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US-08-466-163B-7
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79 NPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCAR---WDYGTTYGYFDVWGQGTTV 135
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| Patent No. 5948658
| GENERAL INFORMATION:
| APPLICANT: Landry Donald, W. TITLE OF INVENTION:
| TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Cooper and Dunham LLP STREET: 1185 Avenue of the Americas CITY: New York STATE: New York
                                                                                       STRUKENLI INFURMATION:

APPLICANT: Jardieu, Paula M.

APPLICANT: Jardieu, Leonard G.

TITUE OF INVENTION: Anti-Igs Antibodies (as amended);
FILE REFERENCE: POT18P2CIDICIUS
CURRENT APPLICATION NUMBER: US/09/925,179

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 08/466,163

PRIOR APPLICATION NUMBER: US 08/466,163

PRIOR APPLICATION NUMBER: US 08/465,617

PRIOR APPLICATION NUMBER: US 08/185,899

PRIOR FILING DATE: 1995-03-15

PRIOR APPLICATION NUMBER: US 07/879,495

PRIOR APPLICATION NUMBER: US 07/744,768

NUMBER OF SEQ ID NOS: 68

NUMBER OF SEQ ID NOS: 68
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-UUN-1996
CLASSIFICATION: 435
                      \Sigma_quence 7, Application US/09925179
Patent No. 6914129
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-925-179-7
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131, App
10, Appl
29, Appl
19, Appl
3, Appl
69, Appl
69, Appl
21, Appl
22, Appl
22, Appl
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470.686 Million cell updates/sec
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/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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1 MRVLILLWLFTAFPGILSDV......WDYGTTYGYFDVWGQGTTVT 136
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                                                                                                                     May 19, 2006, 17:47:39 ; Search time 133.841 Seconds
GenCore version 5.1.8
(c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published_Applications_AA_Main:*
                                                                                                                                                                                                                                                                                                                                                      2097797 segs, 463214858 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                         US-09-889-936A-6
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Match Length DB
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86.8%; Pred. No. 2e-49;
ive 6; Mismatches 12; Indels
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Publication No. US20050152907A1
GENERAL INFORMATION:
GENERAL ILANG, TONY W.
APPLICANT: LOO, Deryk T.
APPLICANT: X1aolin
TITLE OF INVENTION: THERETO
                                                  US-10-568-237-7
US-09-940-7278-13
US-10-713-248-3
US-10-713-248-7
US-10-713-248-7
US-10-735-916A-71
US-10-732-916A-77
US-10-371-797-17
US-10-371-797-17
US-10-173-996-2
US-10-173-996-2
US-10-791-619-2
US-10-791-619-2
US-09-802-076-5
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121 YDVGYFDYWGQGTTLT 136
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Best Local Similarity 86.8
Matches 118; Conservative
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-791-551-109
$2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000 $2000
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TYPE: PRT
ORGANISM: Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYG 120
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COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFFWARE: PATENTIN Release #1.0, Version #1.30
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/10/837,904
FILING DATE: 04-May-2004
CLASSIFICATION: CUNKnown>
PRIOR APPLICATION NUMBER: US/09/114,285
FILING DATE: 13-Jul-1998
APPLICATION NUMBER: US 08/436,717
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: US 08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: US 08/137,117
FILING DATE: 24-APR-1992
APPLICATION NUMBER: US 08/137,117
FILING DATE: 19-FEB-1992
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Best Local Similarity 87.5%; Pred. No. 1.2e-48;
Matches 119; Conservative 6; Mismatches 10; Indels
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Publication No. US20050142635A1
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
SATO, Koh
BENDIG, Mary Margaret
JONES, Steven Tarran
SALDANHA, Jose William
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
INTERLEUKIN-6 RECEPTOR
FILE REFERENCE: 415072002700
CURRENT APPLICATION NUMBER: US/10/943,640
FUNEBRY FILING DATE: 2004-09-17
PRIOR APPLICATION NUMBER: US 60/504,441
PRIOR FILING DATE: 2003-09-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 468
TYPE: PRI
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; OTHER INFORMATION: Synthetic Construct
US-10-943-640-4
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CARDESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
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121 YA-DYFDYWGQGTTLT 135
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US-10-837-904-31
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61 GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNOFFLOLNSVTSEDTATYYCARWDYG 120
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APPLICANT: HANNA, NABIL
TITLE OF INVENTANCO: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
TITLE OF INVENTO: 307003/0277869
CURRENT APPLICATION NUMBER: 08/09/791,551
CURRENT APPLICATION NUMBER: 60/185,390
PRIOR APPLICATION NUMBER: 60/233,625
PRIOR PILING DATE: 2000-02-28
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 119
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Indels
                                                                                                                                                                                                                                                                                                                                                                                          79.8%; Score 588; DB 5;
83.8%; Pred. No. 1.2e-45;
tive 8; Mismatches 12
FILING DATE: 25-APR-1991
ATTORNEY/ABGNI INFORMATION:
NAME: Wegner, Harcld C.
REGISTRATION NUMBER: 25,258
REFRENCE/DOCKET NUMBER: 53466/234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5399
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERIFITCS:
                                                                                                                                                                                                                              LENGTH: 137 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECTLE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-791-551-119; sequence 119, Application US/09791551; Publication No. US20030235584A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 -YGTTYGYFDVWGQGTTVT 136
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Best Local Similarity 78.4%;
Matches 109; Conservative
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PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PATENTIN Ver. 3.3
SEQ ID NO 52
LENGTH: 127
PRIOR APPLICATION NUMBER: FR 0205753
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APPLICANT: TeGenero GmbH
APPLICANT: TeGenero AG
APPLICANT: HUNIG, Thomas
                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Mus musculus
US-11-012-353-52
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ORGANISM: Artificial
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US-10-389-679-12
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                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-11-012-353-52
; Sequence 52, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORTAIL, NATHALIE
; APPLICANT: CORTAIL, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: LEGER, OLIVIER
; APPLICANT: LEGER, OLIVIER
; APPLICANT: LEGER, OLIVIER
; TITLE OF INVENTION: NOVEL ANTI-IGP-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-196
; FILE REFERENCE: 017753-196
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR PELLING DATE: 2003-12-16
; PRIOR PELLING DATE: 2003-12-16
; PRIOR PELLING DATE: 2003-07-11
; PRIOR FILING DATE: 2003-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LLTAIPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMG 60
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           RESULT 5

US-40-735-916A-52

Sequence 52, Application US/10735916A

Sequence 52, Application US/10735916A

Sequence 52, Application No. US20050084906A1

GENERAL INFORMATION:
APPLICANT: CORVALION:
APPLICANT: CORVALIA. Nathalie
APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: BCK, Alain
APPLICANTON NUMBER: US/10/735,916A
APPLICATION NUMBER: COT/FR 03/00 178
ARIOR FILING DATE: 2003-07-11
BRIOR PILING DATE: 2003-01-20
APRIOR PILING DATE: 2003-01-20
APRIOR PILING DATE: 2002-01-18
APRIOR PIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Mus musculus
US-10-735-916A-52
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TYPE: PRT
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Will-10-310-674A-36
Sequence 36, Application US/10310674A
Sequence 36, Application US/10310674A
Sequence 36, Application US/10310674A
Sequence 36, Application US/2030166860A1
GENERAL INFORMATION:
TITLE OF INVENTION: Peptide Or Protein Containing A C'-D Loop Of The CD28 Receptor TITLE OF INVENTION: Pemily
FILE REPERENCE: 00140/004001
CURRENT APPLICATION NUMBER: US/10/310,674A
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.2
SEQ ID NO 36
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                                                                                                                                      9 LFTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFPGNKLEWMG
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   Length 127;
Query Match 75.2%; Score 554; DB 6; Length 12 Best Local Similarity 82.0%; Pred. No. 1.4e-42; Matches 105; Conservative 6; Mismatches 13; Indels
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US-10-310-674A-36
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APPLICANT: Tedenero AG
APPLICANT: Hanke, Thomas
APPLICANT: Hanke, Thomas
APPLICANT: Hanke, Thomas
APPLICANT: Hanke, Thomas
TITLE CANT: Lin, Chia-Huey
TITLE OF INVENTION: USE OF A CD28 BINDING PHARMACEUTICAL SUBSTANCE FOR MAKING A
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION WITH DOSIS DEPENDENT EFFECT
FILE REFERENCE: 7003/25, TEG/US/0407
CURRENT APPLICATION NUMBER: US/10/946,836A
CURRENT FILING DATE: 2004-09-22
PRIOR APPLICATION NUMBER: DE 103 45 008.4
PRIOR FILING DATE: 2003-09-22
PRIOR FILING DATE: 2003-09-22
PRIOR FILING DATE: 2003-10-20
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTING DATE: 2003-10-20
SOFTWARE: PATENTING DATE: 2013-10-20
SOFTWARE: PATENTING DATE: 2013-11-20
LENGTH: 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: monoclonal antibody 9D7 partial sequence US-10-946-836A-12
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; Sequence 30, Application US/11035599
; Publication No. US20050158829A1
; GENERAL INFORMATION:
; APPLICANT: Fandl, James
; APPLICANT: Chen, Gang
; APPLICANT: Aldrich, Thomas F.;
; TITE OF INVENTION: Activating Receptors
; TITE OF INVENTION: Activating Receptors
; FILE REPERENCE: 1080A
; CURRENT APPLICATION NUMBER: US/11/035,599
; CURRENT FILING DATE: 2005-01-14
; PRIOR FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 53
; SOFFWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
... LENDTH: 730
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial
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US-11-035-599-30
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Best Local &
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TITLE OF INVENTION: Use of a CD28 Binding Substance for Making a Pharmaceutical TITLE OF INVENTION: Composition FILE REPERENCE: 00140/009001, TEG/US/302 CURRENT APPLICATION NUMBER: US/10/389,679 CURRENT FILING DATE: 2003-03-13 PRIOR APPLICATION NUMBER: DE 102 12 108.7 PRIOR PLICATION DATE: 2002-03-13 NUMBER OF SEQ ID NOS: 19 SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Publication No. US2006008457A1

Sublication No. US2006008457A1

GENERAL INFORMATION:

APPLICANT: TedGenero AG

APPLICANT: TedGenero AG

TITLE OF INVENTION: USE OF AN EFFECTIVE SUBSTANCE BINDING TO CD28 FOR PRODUCING

TITLE OF INVENTION: USE OF AN EFFECTIVE SUBSTANCE BINDING TO CD28 FOR PRODUCING

TITLE OF INVENTION: USE OF AN EFFECTIVE SUBSTANCE BINDING TO CD28 FOR PRODUCING

TITLE OF INVENTION: USE OF AN EFFECTIVE SUBSTANCE BINDING TO CD28 FOR PRODUCING

TITLE OF INVENTION: USE OF AN EFFECTIVE SUBSTANCE BINDING TO CD28 FOR PRODUCING

FILE REFERENCE: TEG/US/0409

CURRENT APPLICATION NUMBER: US/10/988,207

PRIOR PELICATION NUMBER: DE 103 52 900.4

PRIOR FILING DATE: 2003-11-11

NUMBER OF SEQ ID NOS: 28

SEQ ID NO 12

LENGTH: 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NPSLKSRISITRDISKNQFFLQLNSVTTEDTATYYCARDWPRPSYWYFDVWGAGTTVT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 NPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYGTTYGYFDVWGQGTTVT 136
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Pred. No. 1.1e-41;
4; Mismatches 11; Indels
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Pred. No. 1.1e-41;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 j OTHER INFORMATION: mab 5.11A partial sequence
US-10-988-207-12
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87.3%;
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87.3%;
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                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1). (121)
; OTHER INFORMATION: mab
US-10-389-679-12
                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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Gaps

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80 PSLRSRISFTRDTSKNOFFLOLNSVTSEDTATYYCARWDYGTTYGYF--DVWGQGTTVT 136
                                                                                                                                                                                94 PSLKSRISITRDTSKNQFFLQLNSVTAEDTATYYCARY-YGSSYNYYGMDYWGQGTSVT 151
                                                                             20 VOLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFPGNKLEWMGYISYSGFTSYN
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DB 6; Length 730;
                                     Indels
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US-09-874-141-53
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                                                                      Fequence 31, 4
Publication No. US200501588291
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Eandl, James
APPLICANT: Papadopoulos, Nicholas
APPLICANT: Aldrich, Thomas F.
ITLE OF INVENTION: Fusion Polypeptides Capable of
ITLE OF INVENTION: Activating Receptors
FILE REFERENCE: 1080A
CURRENT APPLICATION NUMBER: US/11/035,599
CURRENT FILING DATE: 2005-01-14
PRIOR APPLICATION NUMBER: 60/536,968
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fandl, James
APPLICANT: Fandl, James
APPLICANT: Pandl, James
APPLICANT: Pandl, James
APPLICANT: Papadopoulos, Nicholas
APPLICANT: Aldrich, Thomas F.
TITLE OF INVENTION: Fusion Polypeptides Capable of
TITLE OF INVENTION: Activating Receptors
FILE REFERENCE: 1080A
CURRENT RILING DATE: 2005-01-14
PRIOR APPLICATION NUMBER: 60/536,968
PRIOR RILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , 8e-40;
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Publication No. US20050158829A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 84.09
Matches 100; Conservative
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US-11-035-599-29
                                     RESÚLT 12
US-11-035-599-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 VKLEESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYINYSGITSYN 93
                                                      80 PSLRSRISFIRDTSKNQFFLQLNSVTSEDTATYYCARWDYGTTYGYF--DVWGQGTTVT 136
                                                                                  94 PSLKSRISITRDISKNOFFLQLNSVTAEDTATYYCARY-YGSSYNYYGMDYWGQGTSVT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPOSITIONS
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Publication No. US20030012781A1

Publication No. US20030012781A1

GENERAL INFORMATION:

APPLICANT: ANDERSON, DARRELL

APPLICANT: PAN, LI-ZHEN

APPLICANT: PANNA, NABIL

APPLICANT: PANNA, NABIL

APPLICANT: RASTETER, WILLIAM S.

TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPC, TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF

FILE REPERENCE: 037003-0280632

CURRENT FILING DATE: 2001-06-06

PRIOR APPLICATION NUMBER: 60/209,584

PRIOR APPLICATION NUMBER: 60/209,584

PRIOR APPLICATION NUMBER: 60/209,584

PRIOR FILING DATE: 2000-06-06

NUMBER OF SEQ ID NOS: 53

SOFTWARE PATENTING DATE: 2010-06-06

NUMBER OF SEQ ID NOS: 53

SEQ ID NO 53

LENGTH: 140
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US-11-035-599-28
Sequence 28, Application US/11035599
Publication No. US20050158829A1
GENERAL INPORMATION:
APPLICANT: Fandl, James
APPLICANT: Chen, Gang
APPLICANT: Papadopoulos, Nicholas
APPLICANT: Palarich, Thomas F.
TITLE OF INVENTION: Fusion Polypeptides Capable of
FILE REFERENCE: 1080A
CURRENT APPLICATION NUMBER: US/11/035,599
CURRENT FILING DATE: 2004-01-14
PRIOR FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
73.2%; Score 539.5; DB 6;
Best Local Similarity 84.0%; Pred. No. 1.9e-40;
Matches 100; Conservative 11; Mismatches 5;
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Pred. No. 7.6e-41;
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76.58;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
COTHER INFORMATION: Synthetic US-11-035-599-28
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CRGANISM: Homo Bapiens
US-09-874-141-53
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Best Local Similarity
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| Matches | 104; | Conservative | 12; | Mismatches | 19; | Indels | 1; | Gaps | 1; | Gapt | 1; | Gapt
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Search completed: May 19, 2006, 17:52:56 Job time : 134.841 secs

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TYPE: PRT ORGANISM: Artificial sequence
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Best Local Similarity 79.7%;
Matches 94; Conservative
US-11-219-121-11
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Sequence 18, Appl
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                                                                                     May 19, 2006, 17:49:02; Search time 6.47619 Seconds (without alignments) 44.858 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                             FEMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/VS07_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                                                                                                                                                                   1 MRVLILLWLFTAFPGILSDV......WDYGTTYGYFDVWGQGTTVT 136
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            GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-219-121-13
US-11-211-917-30
US-11-211-917-70
US-11-211-917-142
US-10-981-300-54
US-10-981-300-54
US-10-991-300-54
US-10-991-300-54
US-11-211-917-26
US-11-211-917-26
US-11-211-917-26
US-11-211-917-26
US-11-211-917-26
US-11-21-918-42
US-11-254-182-43
US-11-211-917-22
US-11-211-917-22
                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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US-11-211-917-108
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Maximum Match 100%
Listing first 45 summaries
                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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737
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390
386.5
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Maximum DB e
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US-11-219-121-30
US-10-983-104-8
US-11-219-563-84
US-11-219-563-89
US-11-219-563-90
US-11-106-762-25
US-11-254-679-15
                                                                                                  US-11-154-103-10
US-11-211-917-116
US-11-211-917-78
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US-11-211-917-117
US-11-230-593A-31
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US-11-106-762-34
                                                                                                                                          US-11-106-762-36
US-11-230-593A-33
                                                                                                                                                                            ALIGNMENTS
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RESULT 1

US-11-219-121-11

US-11-219-121-11

Sequence 11. Application US/11219121

Publication No. US20060093601A1

GENERAL INFORMATION:

APPLICANT: Fong, Sherman

APPLICANT: Dennis Mark S.

TITLE OF INVENTION: HUMANIZED ANTI-BETA7 ANTAGONISTS AND USES THEREFOR

FILE REFERENCE: P2159R1

CURRENT FILING DATE: 2005-09-02

PRIOR APPLICATION NUMBER: US 60/607,377

PRIOR PILING DATE: 2004-09-03

NUMBER OF SEQ ID NOS: 68

SEQ ID NO 11

LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFPGNKLEWMGYISYSGFTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Gaps
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Pred. No. 6.7e-31;
8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: sequence is synthesized
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78

53

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79 NPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYGTTYGYFDVWGQGTTVT 136
                                  60 NPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCAMTG---SSGYFDFWGPGTMVT 114
                                                                                                                                                         RESULT 2
US-11-219-121-13
US-11-219-121-13
Sequence 13, Application US/11219121
Publication No. US20060093601A1
GENERAL INFORMATION:
APPLICANT: Fong, Sherman
APPLICANT: Dennis Mark S.
TITLE OF INVENTION: HUMANIZED ANTI-BETA7 ANTAGONISTS AND USES THEREFOR
FILE REFERENCE: P2159R1
CURRENT APPLICATION NUMBER: US/11/219,121
CURRENT FILING DATE: 2005-09-02
CURRENT FILING DATE: 2004-09-03
PRIOR FILING DATE: 2004-09-03
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TYPE: PRT
ORGANISM: Homo sapiens
US-11-211-917-70
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; ORGANISM: Homo sapiens
US-11-211-917-86
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Best Local Similarity
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US-11-211-917-86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 LWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGGSIRS-YYWTWIRQPPGK 62
                                                                                                                                                                                                                                                  19 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFPGNKLEWMGYISYSGFTSY 78
                                                                                                                                                                                                                                                                                                                         1 EVQLQESGPGLVKPSQSLSLTCSVTGFFITNNY-WGWIRKFPGNKMEWMGYISYSGSTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 LWLF---TAFP-GILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFPGN
                                                                                                                                                                                                            4; Gaps
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                                                                                                                                                                       66.6%; Score 491; DB 7; Length 146; 79.7%; Pred. No. 8.1e-31; Indels Live 8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOS-11-211-31/-30, Application US/11211917
FUDLICATION NO. US20060093600A1
GENERAL INFORMATION:
APPLICANT: BEDIAN, VAHE
APPLICANT: GLADUE, ROWALD P.
APPLICANT: GLADUE, ROWALD P.
APPLICANT: GLADUE, ROWALD P.
APPLICANT: GLADUE, ROWALD P.
APPLICANT: FENG, XIAO-CHI
APPLICANT: FENG, XIAO-CHI
APPLICANT: FENG, XIAO-CHI
APPLICANT: FENG, XIAO-CHI
APPLICATION NUMBER: US/11/211,917
CURRENT APPLICATION NUMBER: US/10/292,088
PRIOR APPLICATION NUMBER: 60/248,980
PRIOR PILING DATE: 2002-11-09
PRIOR PRLING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PARCHIN Ver. 2.1
SEQ ID NO 30
LENGTH: 466
                                                                                                              OTHER INFORMATION: sequence is synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 70, Application US/11211917; Publication No. US20060093600A1; CENERAL INFORMATION VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: CORVALAN, JOSE
                                                           TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : || |||||||||
123 NFNYFHQWGQGTLVT 137
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NUMBER OF SEQ ID NOS:
SEQ ID NO 13
LENGTH: 146
                                                                                                                                                                       Query Match
Best LJcal Similarity
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US-11-211-917-30
                                                                                                                                   US-11-219-121-13
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                                                                                              FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGGSI-RGYYWSWIRQPPGK 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 LWLF---TAFP-GILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFPGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.5%; Score 424; DB 7; Length 466; 64.7%; Pred. No. 2e-25; tive 16; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                              58.2%; Score 429; DB 7; Length 46 ilarity 65.4%; Pred. No. 8.5e-26; Conservative 15; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFOGRATION:
GENERAL INFOGRATION:
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: GORVALAN, JOSE
APPLICANT: CORVALAN, JOSE
THE REFERENCE: ANTIBODIES TO CD40
TITLE OF INVENTION: ANTIBODIES TO CD40
TITLE REFERENCE: ABX-PP/3 US
CURRENT APPLICATION NUMBER: US/11/211,917
CURRENT FILING DATE: 2005-08-25
PRIOR PILING DATE: 2002-11-08
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
SPIOR FILING DATE: 2001-11-09
SPIOR FILING DATE: 2001-11-09
SOFTWARE: PATENTIN VOX: 147
SOFTWARE: PATENTIN VOX: 147
                                                                      CURRENT APPLICATION NUMBER: US/11/211,917
CURRENT FILING DATE: 2005-08-25
PRIOR APPLICATION NUMBER: US/10/292,088
PRIOR FILING DATE: 2002-11-08
PRIOR PILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SEQ ID NO 70
APPLICANT: FENG, XIAO
TITLE OF INVENTION: ANTIBODIES TO CD40
FILE REFERENCE: ABX-PF/3 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 86, Application US/11211917; Publication No. US20060093600A1; GENERAL INFORMATION:
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123 -DYGWFAPWGQGTLVT 137
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Best Local Similarity 64.78
Marches 88; Conservative
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20 VQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQFPGNKLEWMGYISYSGFTSYN 79
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62 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-----TGDYFDYWGQGTLVT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 PSLRSRISFTRDISKNOFFLQLNSVISEDTATYYCARWDYGTTYGYFDVWGQGTTVT 136
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; Bublication No. US2006009359A1
; GENERAL INFORMATION:
; APPLICANT: GLORGIO SENALDI
; APPLICANT: GLORGIO SENALDI
; APPLICANT: GADI GAZIT-BORNSTEIN
; TITLE OF INVENTION: FOR MAKING AND USING THE SAME
; TITLE OF INVENTION: FOR MAKING AND USING THE SAME
; FILE REFERENCE: ABGX-005
; CURRENT FILING DATE: 2004-11-03
; UNDRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENTH: 443
                                                                                                                                                   Sequence 5.4 Application US/10981300
; Publication No. US20060093599A1
; GENERAL INPORMATION:
APPLICANT: GIORGIO SENALDI
; APPLICANT: GADI GAZIT-BORNSTEIN
; TITLE OF INVENTION: APOR MAKING AND USING THE SAME
; TITLE OF INVENTION: FOR MAKING AND USING THE SAME
; FILE REFERENCE: AGGX-005
; CURRENT APPLICATION NUMBER: US/10/981,300
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 118
; TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 56.7%; Score 418; DB 6; Length 11 Best Local Similarity 68.4%; Pred. No. 1.6e-25; Matches 80; Conservative 16; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-981-300-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: homo sapien
US-10-981-300-20
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US-11-211-917-109
                                                                                                              RESULT 8
US-10-981-300-54
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VQLQESGPGLVKPSETLSLTCTVSGGSISS-YYWSWIRQPPGKGLEWIGYIYYSGSTNYN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYY 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-10-90-10
Sequence 51, Application US/10981300
Sequence 51, Application US/10981300
Publication No. US20060093599A1
GENERAL INFORMATION:
APPLICANT: GIORGIO SENALDI
TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND STILE REFERENCE: ASSC.005
CURRENT FILING DATE: 2004-11-03
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FREEERING FOR MAINDOWN Version 4.0
SOFTWARE: FREEERING FOR Windows Version 4.0
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                                                                                                                                                                                                                                                                    APPLICANT: BEDIAM, VAHE
APPLICANT: GLAUUE, RONALD P.
APPLICANT: GLAUUE, RONALD P.
APPLICANT: GORVALAM, JOSE
APPLICANT: JIA, XIAO-CHI
APPLICANT: JIA, XIAO-CHI
APPLICANT: FENG, XIAO
TITLE OF INVENTION: ANTIBODIES TO CD40
TITLE OF INVENTION: ANTIBODIES TO CD40
TITLE REFERENCE: ABX-PP3 US
CURRENT APPLICATION NUMBER: US/11/211,917
CURRENT FILING DATE: 2005-08-25
PRIOR FILING DATE: 2002-11-08
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SECTION 142
                                                                                                                                                                                       Sequence 142, Application US/11211917
Publication No. US20060093600A1
GENERAL INFORMATION:
        121 TTYGYFDVWGQGTTVT 136
                                                        123 -DYGWFAPWGQGTLVT 137
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US-10-981-300-51
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ORGANISM: Homo sapiens
                                                                                                                                                                    US-11-211-917-142
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Publication No. US20060093600A1

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2 VQLQESGPGLVKPSETLSLTCTVSGGSI-RGYYWSWIRQPPGKGLEWIGYIYYSGSTNYN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 VOLOESGPGLVKPSOSLSLTCSVTGYSITSGYAWNWIRQFPGNKLEWMGYISYSGPTSYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Gaps
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                                                                                                                                             APPLICANT: BEDIAN, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: JA, XIAO-HI
APPLICANT: FENG, XIAO-HI
TITLE OF INVENTION: ANTIBODIES TO CD40
TITLE REPERBNCE: ABX-PF/3 US
CURRENT APPLICATION NUMBER: US/11/211,917
CURRENT FILING DATE: 2002-08-25
PRIOR FILING DATE: 2002-11-08
PRIOR FILING DATE: 2002-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENT ON NOSE: 2011-109
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENT ON NOSE: 121
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 66, Application US/11211917
Sequence 66, Application US/11211917
CENERAL INFORMATION:
APPLICANT: BEDIAM, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: JIA, XIAO-CHI
APPLICANT: JIA, XIAO-CHI
APPLICANT: JIA, XIAO-CHI
APPLICANT: JIA, XIAO-CHI
CURRENT APPLICATION NUMBER: US/11/211,917
CURRENT FILING DATE: 2005-08-25
PRIOR FILING DATE: 2005-01-08
PRIOR FILING DATE: 2002-11-08
PRIOR FILING DATE: 2002-11-08
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENTIN UNMBER: 60/348,980
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENTIN OF SEQ ID NOS: 21
                                        US-11-211-917-98
, Sequence 98, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSLRSRISFTRDTSKNOFFLQLNSVTSEDTATYYCAR-WDYGTTYGYFDVWGQGTTVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 PSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYGTTYGYFDVWGQGTTVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-DYGGN-SYFDYWGQGTLVT 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 56.6%; Score 417.5; DB 7; Length Best Local Similarity 70.1%; Pred. No. 1.8e-25; Matches 82; Conservative 15; Mismatches 17; Indels
GENERAL INFORMATION:
APPLICANT: BEDIAN, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
TYLE APPLICANT: FENG, XIAO-CHI
APPLICANT: FENG, XIAO-CHI
TITLE REPERENCE: ABX-PF/3 US
CURRENT APPLICATION NUMBER: US/11/211,917
CURRENT FILING DATE: 2002-08-25
PRIOR FILING DATE: 2002-11-09
PRIOR FILING DATE: 2002-11-09
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PRECENT IN VERSE: 2010-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PRECENT IN VERSE: 2010-11-09
LENGTH: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BEDIAN, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: JIA, XIAO-CHI
APPLICANT: JIA, XIAO-CHI
APPLICANT: FENG, XIAO
TITLE NE FRENCTION: ANTIBODIES TO CD40
FILE REFRENCE: ABX-PP/3 US
CURRENT APPLICATION NUMBER: US/11/211,917
CURRENT APPLICATION NUMBER: US/10/292,088
FRIOR FILING DATE: 2002-11-08
FRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SEQ ID NO 26
LENGTH: 121
TYPE: PRT
TYPE: PRT
VORGANISM: HOMO Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26, Application US/11211917
Publication No. US20060093600A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-11-211-917-109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 PSLRSRISFIRDISKNOFFLQLNSVISEDIATYYCARWDYGTIYGYFDVWGQGTIVT 136
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                                                                                                          RESULT 14
US-10-981-300-53
Sequence 53, Application US/10981300
Publication No. US2060093599A1
GENERAL INFORMATION:
APPLICANT: GIORGIO SENALDI
TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
TITLE OF INVENTION: FOR MAKING AND USING THE SAME
CURRENT APPLICATION NUMBER: US/10/981,300
CURRENT FILING DATE: 2004-11-03
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 53
LENGTH: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 55.6%; Score 409.5; DB 6; Length 115; Best Local Similarity 67.5%; Pred. No. 6.7e-25; Matches 79; Conservative 17; Mismatches 14; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 55.2%; Score 407; DB 7; Length 121; Best Local Similarity 68.1%; Pred. No. 1.1e-24; Matches 81; Conservative 15; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BEDIAM, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: GORVALAN, JOSE
APPLICANT: JIA, XIAO-CHI
APPLICANT: JIA, XIAO-CHI
APPLICANT: FENG, XIAO
TITLE OF INVENTION: ANTIBODIES TO CD40
FILE REFERENCE: ABX-PF/3 US
CURRENT APPLICATION NUMBER: US/10/292,088
FRIOR APPLICATION NUMBER: US/10/292,088
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SEQ ID NO 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 82, Application US/11211917; Publication No. US20060093600A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CORGANISM: Homo sapiens
US-11-211-917-82
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Search completed: May 19, 2006, 17:53:13 Job time : 7.47619 secs

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Biocceleration Ltd.
GenCore version (c) 1993 - 2006
           Copyright
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- protein search, using sw model OM protein May 19, 2006, 17:34:57; Search time 135.333 Seconds (without alignments) 391.900 Million cell updates/sec Run on:

US-09-889-936A-8 Title: Perfect score:

1 SRGDIVMTQSPSSLSVSAGE......CQNDHIYPYTFGGGTKLEIK 116 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2589679 seqs, 457216429 residues Searched:

2589679 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp20028:* geneseqp2003as:* geneseqp2003bs:* geneseqp2006s:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:*geneseqp2001s:* geneseqp2004s:* geneseqp2005s:* A Geneseq 8:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aab15673 Murine 5B	Add94117 Mouse HUI	Adv66167 Human EpC	Adz83525 AntiEpCam	~	~		m	Adv66135 Anti-CD3-	_	•	Aab62864 Anti-SAF-	Aar38603 MCPC ligh	Aar68742 MAb McPC6	Aaw58483 Murine MC	Adio1145 Murine MC	Aar52036 Light cha		Aed64796 Murine an	Aar53802 FAB light	Aaw42468 Fab15 lig	Aap80460 Sequence	Aar39336 scFv frag
SUMMARIES	αı	AAB15673	ADD94117	ADV66167	ADZ83525	AAY17960	ADZ83445	ADV66137	ADV66133	ADV66135	ADZ83436	ADV66116	AAB62864	AAR38603	AAR68742	AAW58483	AD101145	AAR52036	AD032152	AED64796	AAR53802	AAW42468	AAP80460	AAR39336
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*	Query	100.0	89.9	89.9	89.9	89.9	89.9	89.9	89.9	89.9	89.9	89.9	89.1	88.4	88.4	88.4	88.4	88.4	88.4	88.4	88.4	88.3	88.1	88.1
	Score		545	545	545	545	545	545	545	545	545	545	540	536	536	536	536	536	536	536	536	535	534	534
	Result No.		7	٣	4	Ŋ	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

Humani Fab2 1 MAP 26 MAD 26 Staph MAD 16 Plasmi 1 461 1 1461 1 1461 Natiab Mutine Mutine Mutine Mutine Mutine Mutine Mutine Mutine Mouse	Aed41851 Mouse pro Aed41871 Mouse pro Adv66175 Human EpC
AARS4102 AAW42467 AAR90834 AAR98479 AAR98479 AAR42452 0 AER80923 AAR80923 AAR80939 AAR90839 AAR90839 AAR90839 AAR90839 AAR90839 AAR9010756 ABO10756 ABR44688 ABC4700 ABR44688 ADC67950	AED41851 AED41871 ADV66175
11111111111111111111111111111111111111	113 9
	85.1 85.1 84.7
4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4 4 2 4 6

## ALIGNMENTS

Mouse; 5B3 antibody; IgG1; piezoelectric immunoassay; small molecule explosive detection; 2,4,6-trinitrotoluene; TNT. Murine 5B3 antibody light chain variable region. AAB15673 standard; protein; 116 AA. (YISS ) YISSUM RES & DEV CO. (YEDA ) YEDA RES & DEV CO LTD. 25-JAN-2000; 2000WO-IL000048. 25-JAN-1999; 99IL-00128212. (first entry) WO200043774-A2. 08-JAN-2001 27-JUL-2000. AAB15673; Mus sp. RESULT 1 AAB15673 

Willner I, Eshhar Z; WPI; 2000-524259/47. N-PSDB; AAA74605. Apparatus for detecting small molecules, especially explosives comprises piezoelectric crystal

Disclosure, Fig 3B, 90pp, English.

The present sequence is the light chain variable region of SB3 antibody. The CDNA encoding this sequence was obtained from total RNA extracted from a SB3 Mybridoma by RT-PCR. SB3 is an iggla mithody derived from a TNP-KLH immunised mouse. Its binding to TNP or DNS antigen can be blocked by very low amounts of TNT and it can therefore be used in a method for detecting small assayed explosive molecules. Molecules are detected using a piezoelectric sensor. Piezoelectric immunassasying in liquid phase allows stationary and flow analysis of an aqueous sample. The method is sufficiently sensitive for detection of low molecular weight molecules

92.9%;

Similarity

Best Local

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a novel grafted antibody or its functional fragment comprising one or more complementarity determining regions (CDRs) of a defined light CDR and a heavy CDR with at least one amino acid (aa) substitution where the antibody has specific binding activity for a cryptic collagen epitope. The growth of all solid tumours requires new blood vessel growth, angiogenesis, inhibition of which is an approach to limiting tumour growth. The invention may allow development of therapeutics with a cytostatic activity as a collagen agonist or antagonist. The invention is useful for diagnosing and treating disorders associated with angiogenesis, tumour growth and/or cancer metastasis. The present sequence of the mouse anti-cryptic collagen site antibody HUIV26 variable region light chain used during the creation of the antibody of the invention.
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                                                                                                                            SRGDIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGV
                                                                                                        1 SRGDIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGV
                                                                                                                                                                            FIRDSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                                                                                 FIRDSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                             grafted antibody, complementarity determining region, CDR, light CDR, heavy CDR, cryptic collagen epitope; solid tumour, new blood vessel growth; anglogenesis; tumour growth; cytostatic, collagen agonist; cancer metastasis; anti-cryptic collagen, antibody; HUIV26; variable region light chain;
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           Mouse HUIV26 variable region light chain partial amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New cryptic collagen antibody with one or more complementarity determining regions, useful for diagnosing and treating disorders associated with angiogenesis, tumor growth and/or cancer metastasis.
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                                 Length 116;
                                                                      Indels
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                                 100.0%; Score 606; DB 3; 100.0%; Pred. No. 2.4e-43;
                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID NO 2; 232pp; English
                                                                                                                                                                                                                                                                                                     ADD94117 standard; protein; 113 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-NOV-2002; 2002WO-US038147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-NOV-2001; 2001US-00995529.
06-DEC-2001; 2001US-00011250.
                                                                                                                                                                                                                                                                                                                                                                          29-JAN-2004 (first entry)
                                                                      Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CELL-) CELL MATRIX INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-513649/48.
                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ADD94116.
 Seguence 116 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003046204-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse; murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-NOV-2001;
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                                   Query Match
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ADD94117
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89.9%; Score 545; DB 7; Length 113;

Query Match

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                                                        63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New pharmaceutical composition having a bispecific single chain antibody construct, useful for preventing, treating or ameliorating a tumorous disease, such as an epithelial or minimal residual cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                        4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
                                                                             1 DIVWTQSPSLLSVSAGEKVTMSCKSSQSLLNSGNQKNYLAWYQQKPGQPPKLLIYGASTR
                                                                                                                                                                                                                                                                                                                            Human EpCAM-specific antibody light chain variable domain - SEQ ID 90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
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                                                                                                                                                                                                                                                                                                                                                    bispecific single chain antibody; epithelial cell adhesion molecule; EpCAM; tumor; cancer; cytostatic; light chain variable region.
                                                                                                                      64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                        61 ESGVPDRFTGSGSGTDFTLISSVQAEDLAVYYCQNDHSYPYTFGGGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 545; DB 9; Length 113;
Pred. No. 3.1e-38;
4; Mismatches 5; Indels
                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wolf A,
Pred. No. 3.16-38;
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U, Baeuerle
                           1; Mismatches
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                                                                                                                                                                                                                                  ADV66167 standard; protein; 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berry M, Offner S,
B, Lenkkeri-Schuetz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAY-2004; 2004WO-EP005687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-2003; 2003EP-00012133.
31-MAY-2003; 2003EP-00012134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.9%;
                                                                                                                                                                                                                                                                                             (first entry)
                           Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ADV66166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004106383-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-DEC-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kufer P, E
Kohleisen E
                                                                                                                                                                                                                                                              ADV66167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                  ADV66167
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RESULT E

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The invention relates to a cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second binding domain. The CD3 specific binding construct above or the construct produced by the process, nucleic acid molecule, vector, or host is useful for the preparation of a pharmaceutical composition for the prevention, treatment, or amelioration of a composition for the prevention, a inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, viral disease, allergic reactions, parasitic reactions, graft-versus-host disease, or host-versus-graft disease, a tumor, an inflammatory disease, an immunological construct is useful for treating, preventing, or ameliorating proliferative disease, a tumor, an inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, viral disease, allergic reactions, parasitic reactions, graft-versus-host disease, or host-versus-graft diseases. The present sequence represents the amino coil sequence of an anti-EpCam single chain antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second binding domain, useful for treating, preventing, or ameliorating, e.g.
                                                                                                                                                                                          neoplasm; inflammation; immune disorder; infection; allergy;
graft versus host disease; Cytostatic; Antiinflammatory;
Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baeuerle P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.9%; Score 545; DB 9; Length 113; 92.0%; Pred. No. 3.1e-38; ive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lenkkeri-Schuetz U, Itin C,
                                                                                                                                                   AntiEpCam single chain antibody SEQ ID NO 147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 8; SEQ ID NO 147; 639pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Williams S;
                                    ADZ83525 standard; protein; 113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              15-OCT-2004; 2004WO-EP011646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2003; 2003EP-00023581
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hofmeister R, Kohleisen
Carr FJ, Hamilton AA, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proliferative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-333494/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MICR-) MICROMET AG.
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                                                                                                                                                                                                                                                                                                                                WO2005040220-A1.
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                                                                                                                                                                                                                                                       EpCam; antibody
                                                                                                                14-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                         06-MAY-2005.
                                                                                                                                                                                                                                                                                            Synthetic.
                                                                           ADZ83525;
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RESULT 4
ADZ83525
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the interies of transfer to a mercing of the comparing bitter domains to state the capacity of binding to a predetermined epitope when positioned C-terminal of at least one further domain in a recombinant bicostioned C-terminal of at least one further domain in a recombinant bicompulsed on the surface of a biological display system as part of a BSD displayed on the surface of a biological display system as part of a fusion protein for binding to a predetermined epitope, where the fusion protein comprises an additional domain positioned N-terminal of the BSD and an amino acid sequence that mediates anchoring of the fusion protein to the surface of the display system; and (b) identifying a BSD that binds to the predetermined epitope. The method is useful to identify bicomputed to protein antibody state capable of efficiently binding to the corresponding antibody in the protein gradies that comprise antibody successible. The polypeptides or antibodies identified by the method are useful therapeutically and diagnments that bind independently of their position within bifunctional single-chain fusion proteins can be isolated from combinatorial antibody in button method. Sequences AAY17957-965 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phage display system for identification of binding site domains retaining capacity to bind an epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer; autoimmune disease; scFv-antibody; single-chain Fv; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to a method of identifying binding site domains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                      Lutterbuese R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.9%; Score 545; DB 2; Lv 92.0%; Pred. No. 6.7e-38; ive 4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                      Zettl F,
AAY17960 standard; protein; 248 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; Fig 6.6; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      Borschert K,
                                                                                                                                                                                                                                                                                                          98WO-EP007313.
                                                                                                                                                                                                                                                                                                                                              97EP-00120096.
                                                                      (first entry)
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Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse scFV fragments
                                                                                                          Mouse scFV fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                        Raum T,
                                                                                                                                                                                                                                                                                                                                                                                    Д,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                                                                                    (KUFE/) KUFER
                                                                                                                                                                                                                                      WO9925818-A1
                                                                                                                                                                                                                                                                                                            16-NOV-1998;
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                                                                      04-AUG-1999
                                                                                                                                                                                                                                                                          27-MAY-1999.
                                    AAY17960;
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ADZ83445 standard; protein; 497 AA.

4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63

6 8 6

9

bispecific single chain antibody, epithelial cell adhesion molecule, EpCAM, CD3, tumor, cancer; cytostatic.

Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 60.

24-FEB-2005 (first entry)

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The invention relates to a cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second binding domain. The CD3 specific binding construct above or the construct produced by the process, nucleic acid molecule, vector, or host is useful for the preparation of a pharmaceutical composition for the prevention, treatment, or amelioration of a nucleic acid molecule, composition for the prevention, treatment, or amelioration of a disorder, an autonimmune disease, an infectious disease, wiral disease, allergic reactions, parasitic reactions, graft-versus-host disease, or host-versus-graft disease. The cytoxically active CD3 specific binding construct is useful for treating, preventing, or ameliorating construct disease, a tumor, an inflammatory disease, an immunological disorder, an autonimmune disease, an inflammatory disease, viral disease, callergic reactions, parasitic reactions, graft-versus-host diseases, or host-versus-graft diseases. The present sequence represents the amino acid sequence of a CD3 specific binding construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second binding domain, useful for treating, preventing, or ameliorating, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63
                                                                                                      neoplasm; inflammation; immune disorder; infection; allergy;
graft versus host disease; Cytostatic; Antiinflammatory;
Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 545; DB 9; Length 497;
Pred. No. 1.3e-37;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      n B, Lenkkeri-Schuetz U,
Williams S;
                                                                      CD3 specific binding construct SEQ ID NO 67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 67; 639pp; English.
                                                                                                                                                                                                                                                                                            15-OCT-2004; 2004WO-EP011646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.9%;
92.0%;
                                                                                                                                                                                                                                                                                                                                16-OCT-2003; 2003EP-00023581
                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      Hofmeister R, Kohleisen
Carr FJ, Hamilton AA, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proliferative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-333494/34.
N-PSDB; ADZ83444.
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                                                                                                                                                                                                                   WO2005040220-A1
                                    14-JUL-2005
                                                                                                                                                                                                                                                       06-MAY-2005
                                                                                                                                                                                 Synthetic
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 ADZ83445
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ADV66137
ID ADV6
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AC ADV6
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New pharmaceutical composition having a bispecific single chain antibody construct, useful for preventing, treating or ameliorating a tumorous disease, such as an epithelial or minimal residual cancer.

Claim 12; SEQ ID NO 60; 227pp; English.

Raum T;

Wolf A,

Kufer P, Berry M, Offner S, Brischwein K, V Kohleisen B, Lenkkeri-Schuetz U, Baeuerle P;

WPI; 2005-021271/02. N-PSDB; ADV66136

Baeuerle P;

ບັ Itin

(MICR-) MICROMET AG.

26-MAY-2004; 2004WO-EP005687. 31-MAY-2003; 2003EP-00012133. 31-MAY-2003; 2003EP-00012134.

WO2004106383-A1

Unidentified

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The invention comprises a composition that contains a bispecific single chain antibody consisting of at least two domains, where one of domains binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the second domain binds to human OD3 antigen. The bispecific antibody construct of the invention is useful for the prevention, treatment or amelioration of a tumorous disease, such as an epithelial or minimal residual cancer. The present amino acid sequence represents a bispecific single chain antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bispecific single chain antibody, epithelial cell adhesion molecule, EpCAM, CD3, tumor, cancer, cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 545; DB 9;
Pred. No. 1.4e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADV66133 standard; protein; 503 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.9%;
92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 500 AA;
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Gaps

; 0

ADV66137 standard; protein; 500 AA

ADV66137

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WPI; 2005-021271/02.
N-PSDB; ADV66134.
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                                                                                                                                                                                                   Sequence 503 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                     The invention comprises a composition that contains a bispecific single chain antibody consisting of at least two domains, where one of domains binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the second domain binds to human CD3 antigen. The bispecific antibody construct of the invention is useful for the prevention, treatment or amelioration of a tumorous disease, such as an epithelial or minimal residual cancer. The present amino acid sequence represents a bispecific single chain antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                      ELVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSGNQKNYLAWYQQKPGQPPKLLIYGASTR 444
                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                          antibody
                                                                                                                                                                                                                                                                                                                                                                                 DIVMTOSPSSLSVSAGEKVTMSCKSSOSLLNSRNOKNYLAWYQQKPGOPPKLLIYGVFIR
                                                                                                                                                       New pharmaceutical composition having a bispecific single chain antibo construct, useful for preventing, treating or ameliorating a tumorous disease, such as an epithelial or minimal residual cancer.
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bispecific single chain antibody; epithelial cell adhesion molecule;
EpCAM; CD3; tumor; cancer; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                           DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                     445 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPYTFGGGTKLEIK 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 58
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                                                                                            Raum T;
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                                                                                                                                                                                                                                                                                                                                      Score 545; DB 9; Length 503;
Pred. No. 1.4e-37;
4; Mismatches 5; Indels
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                                                                                            Wolf A,
                                                                                            ry M, Offner S, Brischwein K, 1
Lenkkeri-Schuetz U, Baeuerle P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kufer P, Berry M, Offner S, Brischwein K, V
Kohleisen B, Lenkkeri-Schuetz U, Baeuerle P;
                                                                                                                                                                                                  Claim 12; SEQ ID NO 56; 227pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADV66135 standard; protein; 503
                      26-MAY-2004; 2004WO-EP005687
                                         31-MAY-2003; 2003EP-00012133 31-MAY-2003; 2003EP-00012134
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 92.0%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-2004; 2004WO-EP005687
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                                                                                                                           2005-021271/02
                                                                       (MICR-) MICROMET AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MICR-) MICROMET AG
                                                                                             Berry M,
                                                                                                                                     N-PSDB; ADV66132
                                                                                                                                                                                                                                                                                                                      Sequence 503 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004106383-A1
                                                                                                        Kohleisen B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
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 09-DEC-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADV66135;
                                                                                            Kufer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
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The invention comprises a composition that contains a bispecific single chain antibody consisting of at least two domains, where one of domains binds to human epithelial cell adhesion wolecule (EpcAM) antigon, and the second domain binds to human CD3 antigen. The bispecific antibody construct of the invention is useful for the prevention, treatment or amelioration of a tumorous disease, such as an epithelial or minimal residual cancer. The present amino acid sequence represents a bispecific single chain antibody of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           444
New pharmaceutical composition having a bispecific single chain antibody construct, useful for preventing, treating or ameliorating a tumorous disease, such as an epithelial or minimal residual cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neoplasm; inflammation; immune disorder; infection; allergy;
graft versus host disease; Cytostatic; Antiinflammatory;
Immunosuppressive; Virucide; Antibacterial; Antlallergic; Antiparasitic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 DIVMTOSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baeuerle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lenkkeri-Schuetz U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

89.9%; Score 545; DB 9;
Best Local Similarity 92.0%; Pred. No. 1.4e-37;
Matches 104; Conservative 4; Mismatches 5;
                                                                                                                                    Claim 12; SEQ ID NO 58; 227pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 58; 639pp; English.
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Carr FJ, Hamilton AA, Williams S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deimmunized construct 4-1xanti-CD3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADZ83436 standard; protein; 515
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The invention relates to a cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second binding domain. The CD3 specific binding construct above or the construct produced by the process, nucleic acid molecule, vector, or host is useful for the preparation of a pharmaceutical proliferative disease, a tumor, an inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, an immunological allergic reactions, parasitic reactions, parasitic reactions, parasitic reactions, parasitic reactions, construct is useful for treating, preventing, or ameliorating
                                                                                                                                                                                                                                                                                                                                     proliferative disease, a tumor, an inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, viral disease, allergic reactions, parasitic reactions, graft-versus-host diseases, or host-versus-graft diseases. The present sequence represents the amino acid sequence of deimmunized construct 4-lxanti-CD3.
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Sequence 515 AA;

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                                                                4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
                                                                                              ELVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSGNQKNYLAWYQQKPGQPPKLLIYGASTR
                                 Gaps
                                                                                                                            DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                            SGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPTFGGGTKLEIK 132
                                 .
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Score 545; DB 9; Length 515;
Pred. No. 1.4e-37;
4; Mismatches 5; Indels
 89.9%;
92.0%;
                                 Matches 104; Conservative
                  Local Similarity
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   Query Match
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bispecific single chain antibody; epithelial cell adhesion molecule; EpCAM; CD3; tumor; cancer; cytostatic. Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 39. ADV66116 standard; protein; 521 AA (first entry) 24-FEB-2005 ADV66116; RESULT 11 ADV66116

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ADV6

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WO2004106383-A1

09-DEC-2004.

26-MAY-2004; 2004WO-EP005687.

31-MAY-2003; 2003EP-00012133.

(MICR-) MICROMET AG

Raum T; Wolf A, Brischwein K, 1 U, Baeuerle P; Lenkkeri-Schuetz Offner S, Kufer P, Berry M, Kohleisen B,

WPI; 2005-021271/02. N-PSDB; ADV66115. New pharmaceutical composition having a bispecific single chain antibody construct, useful for preventing, treating or ameliorating a tumorous disease, such as an epithelial or minimal residual cancer.

Claim 12; SEQ ID NO 39; 227pp; English.

The invention comprises a composition that contains a bispecific single chain antibody consisting of at least two domains, where one of domains binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to sialoadhesin factor-1 (SAF-1) monoclonal antibodies 13G3 and 11G4. A neutrophil-priming dose of SAF-1 agonist antibody or a pharmaceutical composition comprising the antibody is useful for treating or preventing an infectious disease state such as osteomyelitis, deep seated wound infections, sepsis, antibiotic resistent bacterial infection, viral infections and those involving intracellular pathogens and parasites such as Listeria monocytogenes, Salmonella and leishmania in amammal. Nucleic acid sequences encoding the variable light chain and heavy chain peptide sequences are useful for mutagenic introduction of specific changes within the nucleic acid sequences encoding the (complementarity determining regions) CDRs or framework regions, and for incorporation of the resulting modified or fusion nucleic acid sequence into a plasmid for expression. The CDR-encoding regions comprising silent mutations are used in construction of humanized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sialoadhesin factor-1; SAF-1; anti-SAF-1 monoclonal antibody; 13G3; 11G4; osteomyelitis; wound infection; sepsis; Listeria monocytogene; Salmonella; Leishmania; kappa chain variable region; mouse.
second domain binds to human CD3 antigen. The bispecific antibody construct of the invention is useful for the prevention, treatment or amelioration of a tumorous disease, such as an epithelial or minimal residual cancer. The present amino acid sequence represents a bispecific single chain antibody of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New sialoadheisn factor-1 agonist antibody having the characteristic of monoclonal antibody 13G3 or 11G4 for treating ostcomyelitis, deep seated wound infections and antibiotic resistant bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-SAF-1 monoclonal antibody 13G3 kappa chain variable region protein.
                                                                                                                                                                                                                                                                          SO ELVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSGNQKNYLAWYQQKPGQPPKLLIYGASTR
                                                                                                                                                                                                                                              4 DIVMIQSPSSLSVSAGEKVIMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                    SO ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPYTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                              64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
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                                                                                                                                                              Length 521;
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                                                                                                                                                            89.9%; Score 545; DB 9;
92.0%; Pred. No. 1.4e-37;
ive 4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  King AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB62864 standard; protein; 114 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-AUG-2000; 2000WO-US022663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .9-AUG-1999; 99US-0149753P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                      104; Conservative
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                                                                                                                                                                                   Similarity
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                                                                                                                        Sequence 521 AA;
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Best Local (
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Sequence 113 AA;
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15-JUL-1995
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Region
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                                                                                                                                                                                                                    4 DIVMTOSPSSLSVSAGEKVTMSCKSSQSLLNSRNOKNYLAWYQQKPGQPPKLLIYGVFIR
                                                                                                                                                                                                                                            DIVMTQSPSSLSVSAGEKVTMNCKSSQSLLNSGNQKNYLAWYQQKPGQPPKLLIYGASTR
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibodies prepn. used for treatment of auto-immune diseases - by replacement of critical residues to reduce immunogenicity but retain
      antibodies or other engineered antibodies. The present sequence represents anti-SAF-1 monoclonal antibody 13G3 kappa chain variable region amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody; variable domain; light; L; heavy; H; consensus; affinity; antigen; immunogenicity; humanisation; framework.
                                                                                                                                                                                                                                                                                                                           61 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNEHSYPFTFGSGTKLEIK 113
                                                                                                                                                                                                                                                                                                        64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 31. .36 /note= "variation in length of hypervariable loop sequences among antibodies"
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                                                                                                                          Score 540; DB 4; Length 114;
Pred. No. 8.2e-38;
4; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 85; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR38603 standard; protein; 113 AA.
                                                                                                                                 89.1%;
91.2%;
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(first entry)
                                                                                                                                                                      Matches 103; Conservative
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binding affinity, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-213827/26.
                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MCPC light chain.
                                                                                         Sequence 114 AA;
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28-OCT-1993
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                                                                                                                                               9
                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to Cys for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monoclonal antibody; McPC603; disulfide bond; heavy chain; light chain; variable region; Fv; antibody engineering; ligand binding moiety; immunotoxin.
                                                                                                                           1 DIVMTQSPSSLSVSAGERVTMSCKSSQSLLNSGNQKNPLAWYQQKPGQPPKLLIYGASTR
                                                                                                      4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
                                                               Gaps
                                                                                                                                                                                         64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                                                                                                      61 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHSYPLTFGAGTKLEIK 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "residue at position 49 can be changed possible interchain disulfide bond"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "complementarity determining region 2"
                    Length 113;
Score 536; DB 2; Length 11.
Pred. No. 1.8e-37;
....rerches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "Ser to Tyr mutation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "framework region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "framework region 3"
                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               AAR68742 standard; protein; 113 AA
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|abel= CDR2
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/label= CDR1
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/label= CDR3
                  Query Match
Best Local Similarity 91.2%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104. .113
/label= FR4
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'label= FR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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/label= 1
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Search completed: May 19, 2006, 17:40:05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       method comprises administering a cytotoxic protein containing a modified immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig molecule or an immunoconjugate or fusion protein containing an anti-CD5 Ig molecule, and where the modified Ig variable domain comprises at least one of (a) a modified light chain variable region (see AAM58478 or
                                                  New ligand-binding polypeptide(s) - having a disulphide bond linking framework regions of first and second variable regions of ligand binding
                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies with humanised variable regions.
                                                                                                                                The polypeptide given in AAR68742 corresponds to the light chain of MAD MCPC603. This MAD was used to generate a model of MAD B3(Fv), which has been used in the construction of disulfide bond-stabilized Fv fragments used as immunotoxins. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                            DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
                                                                                                                                                                                                                                                                                                      DIVMTQSPSSLSVSAGERVTMSCKSSQSLLNSGNQKNFLAWYQQKPGQPPKLLIYGASTR
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                                                                                                                                                                                                                               SCOPPORFTGSGGTDFTLTISSVQAEDLAVYYCQNDHSYPLTFGAGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanised; human; mouse, CD5; anti-CD5 antibody; immunoglobulin;
depletion; cytotoxic; immunoconjugate; fusion protein; psoriasis;
autoimmune disease; rheumatoid arthritis; type I diabetes.
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                                                                                                                                                                                                                           Length 113;
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                                                                                                                                                                                                                         Score 536; DB 2;
Pred. No. 1.8e-37;
                                                                                                                                                                                                                                                   3; Mismatches
 Brinkmann
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                                                                                                        Disclosure; Page 53; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                            AAW58483 standard; protein; 113
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92WO-US010906.
93US-00082842.
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91.2%;
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B, Jung
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                           WPI; 1995-036408/05
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  ree
                                                                                                                                                                                                 Sequence 113 AA;
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                  or AAMS8481), where AAWS84818 and AAWS8479 are humanised forms of the H65 light and heavy chain variable domains with low risk amino acid substitutions [i.e. low risk of reducing antigen-blading specificity.] and AAWS8480 and AAWS8481 are humanised forms of the H65 light and heavy chain variable domains with moderate risk amino acid substitutions and are present in humanised H65 antibody he3 (ATCC HB 11206). The method is useful for treating autoimmune diseases, especially systemic lupus erythematosus, rheumatoid arthritis, psoriasis or type I diabetes. The present sequence represents the murine MCPC antibody light chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
modified heavy chain variable region (see AAW58479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
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91.2%;
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Best Local (
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

May 19, 2006, 17:40:37 ; Search time 22.0952 Seconds (without alignments) 505.138 Million cell updates/sec

US-09-889-936A-8 Title: Perfect score:

606 1 SRGDIVMTQSPSSLSVSAGE......CQNDHIYPYTFGGGTKLEIK 116 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES	
Result No.	Score	Query	Length	DB	ΙD	Description
	542	89.4	135	7	S38807	Ig light chain V-J
7	536	88.4	112	~	F30538	Ig kappa chain V r
m	536	88.4	112	7	E30538	Ig kappa chain V r
4	531	87.6	113	~	026	kappa
ß	520	85.8	108	N	E30535	kappa chain V
9	515	85.0	107	~	G30535	kappa chain V
7	512	84.5	107	~	F30535	Ig kappa chain V r
80	509	84.0	113	~	PL0263	kappa chain V
თ	208	83.8	107	7	D30535	kappa
	508	83.8	107	7	B30535	kappa chain V
11	503	83.0	105	~	C30535	kappa chain V
12	495	81.7	220	~	A31790	kappa chain
13	485	80.0	214	~	S68212	kappa
14	473.5	78.1	112	N	S43103	kappa chain
	473.5	78.1	113	N	PT0407	light
16	473	78.1	145	~	PL0014	kappa chain pr
17	472.5	78.0	118	N	PT0356	kappa chain
18	470.5	77.6	112	~	PL0265	Ig kappa chain V r
19	469.5	77.5	112	C3	S41393	kappa
20	467.5	77.1	133	~	PS0023	Ig kappa chain pre
21	467	77.1	134	~	PC1214	kappa
22	464.5	76.7	111	~	G30502	kappa chain
23	462	76.2	111	~	803304	kap
24	461	76.1	113	N	JC2270	-6 antibody
25	461	. 76.1	113	N	A49260	monoc
26	460.5	76.0	138	~	S26040	kappa
27	460	75.9	240	7	S06084	
28	459.5	75.8	113	~	PT0408	light
59	457	75.4	113	~	S30520	

kappa	Ig kappa chain pre	kappa	i-Sm	Ig light chain V r	Ig kappa chain V-J	Ig kappa chain V r	Ig kappa chain V r	Ig heavy chain V r	Ig kappa chain - h	Ig kappa chain V-J	Ig kappa chain V-J	Ig kappa chain pre	Ig kappa chain V r	Ig light chain V r	Ig kappa chain - h
K4HULN	K4HU17	K4HUJI	849531	S26336	809970	S34003	834002	S20648	S40364	844119	844116	G33932	830523	PH1047	S40347
1 K4HULN	1 K4HU17	1 K4HUJI	2 849531	2 \$26336	2 \$09970	2 \$34003	2 \$34002	2 \$20648	2 \$40364	2 S44119	2 S44116	2 G33932	2 \$30523	2 PH1047	2 S40347
114 1 K4HULN	134 1 K4HU17	н	7	7	7	7	N	N	~	7	~	~	~	N	رن
	н	133 1	134 2	109 2	112 2	113 2	113 2	94 2	124 2	114 2	114 2	120 2	113 2	103 2	129 2 8
75.4	134 1	74.7 133 1	73.9 134 2	73.8 109 2	73.5 112 2	73.1 113 2	72.9 113 2	72.6 94 2	72.6 124 2	72.4 114 2	72.4 114 2	72.4 120 2	72.1 113 2	72.0 103 2	129 2 8

# ALIGNMENTS

 RESULT 1 \$38807  Ig light chain V-J region - mouse  Ig light chain V-J region - mouse  C.Species: Mus musculus (house mouse) C.Species: Musculus for the mouse for
Query Match 89.4%; Score 542; DB 2; Length 135; Best Local Similarity 91.2%; Pred. No. 8.7e-41; Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 Oy 3 GDIVWTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFI 62 
Qy 63 RDSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYXCQNDHIYPYTFGGGTKLEI 115  :
 RESULT 2 F30538 Ig kappa chain V region (253.15D10) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Accession: F30538 R;Claflin, J.L.; Berry, J. J. Immunol. 141, 4012-4019, 1988 R;Claflin, J.L.; Berry, J. J. Immunol. 141, 4012-4019, 1988 R;Claflin, J.L.; Procession: F30538 R;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneum A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneum A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneum A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneum A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneum A;Title: Genetics of the phosphocholin (sequence not shown; not compared with conceptual trar A;Nolecule type: mRNA A;Residues: 1-112 <cla> A;Cross-references: UNIPARC: UPI0000176CDS A;Cross-references: UNIPARC: UPI0000176CDS G;Superfamily: immunoglobulin vegion; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;16-96/Domain: immunoglobulin homology <imm></imm></cla>

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63 9

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Ig kappa chain V region (2G6) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 21-Jan-2000
C;Accesion: G30535
R;Clafilin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.
J. Immunol. 138, 3060-3068, 1987
A;Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with A;Reference number: A30556; MUID:87196439; PMID:3106498
A;Reference number: A30556; MUID:87196439; PMID:3106498
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                   C.Species: Mus musculus (house mouse)
C.Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 21-Jan-2000
C.Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 21-Jan-2000
C.Accession: E30535
R.Claflin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.
J. Immunol. 138, 3060-3068, 1987
A.Fitele: Somatic evolution of diversity among anti-phosphocholine antibodies induced with A.Reference number: A30556; MUID:87196439; PMID:3106498
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                             DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
                                                          1 DIVWIQSPSSLSVSAGDKVIMSCKSSQSLLNSRNQKWYLAWYQQKPWQPPKLLIYGASTR
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                                                                                                                                       64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                                                          61 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLELK 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: the sequence was determined from the differentiated generic superfamily: immunoglobulin vegion; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin F;16-96/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: the sequence was determined from the differentiated gen
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
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Pred. No. 1.6e-38;
1; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
85.8%; Score 520; DB 2;
Best Local Similarity 92.6%; Pred. No. 6e-39;
Matches 100; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                         Ig kappa chain V region (6D10) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Accession: E30535
A,Status: preliminary
A,Mole type: DNA
A,Residues: 1-108 <CLA>
A,Cross-references: UNIPARC:UPI0000176AED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: UNIPARC: UPI0000176AF6
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1 Similarity 92.5%;
99; Conservative :
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A; Residues: 1-107 < CLA>
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Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                            Ig kappa chain V region (253.12D3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Nus musculus (house mouse)
C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 21-Jan-2000
C;Accession: E30538
R;Clafilu, J.L; Berry, J.
J; Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu A;Reference number: A30534; MUID:89035545; PMID:3141511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ig kappa chain V region (anti-DNA, D20VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
B;Schocosion: Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A;Reference number: PL0231; MUID:90111618; PMID:2104919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
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                                                                                                                  DIVMIQSPSSLSVSAGEKVIMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
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     Length 112;
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Pred. No. 6.8e-40;
4; Mismatches 7; Indels
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A; Readidues: 1-113 <SHL.>
A; Cross-references: UNIPARC:UPI0000176AFB
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;1-27 Region: framework 1
F;16-96/Domain: immunoglobulin homology <IMM>
F;24-40/Region: complementarity-determining 1
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A;Cross-references: UNIPARC:UPIO000176CD4
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <!MM>
Score 536; DB 2; Length 11
Pred. No. 2.4e-40;
2; Mismatches 7; Indels
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Pred. No. 2.4e-40;
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92.0%; Pred. No. 2...
'.. 2; Mismatches
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     88.4%;
92.0%;
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Best Local Similarity 90.3%;
Matches 102; Conservative
Query Match
Best Local Similarity 92.0°
Matches 103; Conservative
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Ig kappa chain V region (7C9) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Accession: D30335
R;Claflin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.
J. Immunol. 138, 3060-3068, 1987
A;Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with A;Reference number: A30556; MUID:87196439; PMID:3106498
A;Reference number: A30556; MUID:87196439; PMID:3106498
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R;Claflin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.
J. Immunol. 138, 3060-3068, 1987
A;Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with A;Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with A;Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with A;Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with A;Reference: Preliminary
A;Molecule type: DNA
A;Residues: 1-107 < CLA>
A;Cross-reference: UNIPARC:UPI0000176AF5
A;Cross-reference: UNIPARC:UPI0000176AF5
A;Cross-reference: UNIPARC:UPI0000176AF5
A;Cross-reference: UNIPARC:UPI0000176AF5
A;Cross-reference: UNIPARC:UPI0000176AF5
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C;Species: Mus musculus (house mouse)
C;Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain V region (2B2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Feb_1989 #sequence_revision 23-Feb-1989 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVMTQSPSSLSVSAXEKVTMSCKSSQSLLNSGNQKNYLAWYQQKPGQPPKLLIYGASTR
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A,Residues: 1-107 <CLA>
A,Crose-references: UNIDARC:UPI0000176AF9
A,Note: the sequence was determined from the differentiated gene
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
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Pred. No. 6.7e-38;
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Best Local Similarity 90.7%; Pred. No. 6.7e-38;
Matches 97; Conservative 2; Mismatches 8;
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91.6%;
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Best Local Similarity 91.6
Matches 98; Conservative
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                                                                                     RESULT 7
F13.535
Ig Asppa chain V region (5G4) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 21-Jan-2000
C;Accession: F30515
R;Claflin, Jl.; Berry, J.; Flaherty, D.; Dunnick, W.
J. Immunol. 138, 3060-3068, 1987
A;Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced wit A;Reference number: A30556; MUID:87196439; PMID:3106498
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PL0263
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Elg Kappa chain V region (anti-DNA, S57VK, S41VK, S54VK, S7VK and S204VK) - mouse (fragme C;Species: Mus musculus (house mouse)
C;Species: I6-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0263
R;Shlomchik, M: Mascelli, M: Shan, H: Radic, M.Z.; Pisetsky, D: Marshak-Rothstein, A J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0263
A;Molecule type: mRNA
A;Residues: 1-113 <SHL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIVMTQSPSSLSVSAGEKVTMNCKSSQSLLNSGNQKNYLAWYQQKPGQPPKLLIYGASTR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHSYPLTFGAG 107
ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHSYPLTFGAG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A)Cross-references: UNIPARC:UPI0000176AFA
A)Note: the sequence was determined from the differentiated gene
C)Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 512; DB 2; Length 107;
Pred. No. 3e-38;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Pred. No. 5.8e-38;
5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-23/Region: framework 1
16-96/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56-62/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.5%;
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Best Local Similarity 86.7%;
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 <CLA>
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Best Local Similarity
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Ig kappa chain V-J region (4B1 VL) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S43103
R;Gilbert, D.; Brard, F.; Margaritte, C.; Delpech, A.; Tron, F.
Submitted to the RMB1 Data Library, March 1994
A;Description: An idiotype D23-bearing polyspecific, murine anti-DNA monoclonal antibody
A;Reference number: S42484
A;Accession: S43103
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-112 <GIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPARC:UP10000116626; EMBL:Z31353; NID:9467574; PIDN:CAA83231.1; PII C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PT040
C;Accession: PT040
C;Accession: D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A;Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibodie
                                                                                                                                            4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63
                                                                                                                                                                             4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
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                                                                                                                                                                                                                                                                                            SCOVPDRFIGSGSGTDFTLTISTVQAEDLADYFCQQHYSTPYTFGGGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCONDHIYPYTFGGGTKLEIK 116
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                             Length 214;
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A;Residues: 1-113 <BEH>
A;Cross-references: UNIPARC:UPI000176A05
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
                                                                                   12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Indels
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A, Accession: PT0407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.1%; Score 473.5; DB 2,
84.1%; Pred. No. 7.5e-35;
tive 6; Mismatches 11;
                          Score 485; DB 2;
Pred. No. 1.4e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.1%; Score 473.5; DB 2
83.2%; Pred. No. 7.6e-35;
iive 7; Mismatches 11
                                                                                   8; Mismatches
                             Score 485;
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                       80.0%;
82.3%;
                                                                                   93; Conservative
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                          Query Match
Best Local Similarity
Matches 93; Conserv
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Matches 9
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                 A)Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced wit A; A; Reference number: A30556; MUID:87196439; PMID:3106498
A; Accession: C30535
A; Status: preliminary
A; Molecule: preliminary
A; Residuale: 1-105 < CLLA>
A; Residuale: 1-105 < CLLA>
A; Cross-references: UNIPARC:UPI0000176AF4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-220 <SCH:
A;Cross-references: UNIPARC:UPI0000114E12; GB:M23626; GB:J04061; NID:g533234; PIDN:AAA39
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
C;Accession: S68312
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
Ests Lett. 375, 273-276, 1995
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A;Reference number: S68211; MUID:96085223; PMID:7498516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain V region (17/9) - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Species: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000 C; Accession: A31790 R; Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A. J. Biol. Chem. 263, 17100-17105, 1988 A; Title: Preliminary crystallographic data, primary sequence, and binding data for an a A; Reference number: A92686; MUID:89034213; PMID:3182835
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A,Status: preliminary; nucleic acid sequence not shown
A,Nolecule type: mRNA
A,Residues: 1-214 <TAK>
A,CRSIGUES: 1-214 <TAK>
A,CRSIGUES: 1-214 <TAK>
C,CSSUPETERIORS: UNIPARC: UPI00017697E; EMBL: D29668
C,Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                         83.0%;
91.4%;
J. Immunol. 138, 3060-3068, 1987
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Best Local Similarity 91...
Local Similarity 91...
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nes 95; Conserv
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61 ECGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNL-YTFGGGTKLEIK 112

Search completed: May 19, 2006, 17:47:24 Job time : 23.0952 secs

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### November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions <code>:rnpbm</code> (Published_Applications_NA_Main) and <code>.rnpbm</code> (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions <code>.rapbm</code> (Published_Applications_AA_New).



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QEKBOS_MOUSE
QEKBOS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                         1 SRGDIVMTQSPSSLSVSAGE.......CQNDHIYPYTFGGGTKLEIK 116
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                     5.1.8
Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                            2849598 segs, 925015592 residues
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KV4A_HUMAN
KV4C_HUMAN
KV4B_HUMAN
KV4D_HUMAN
KV4D_HUMAN
KV1A_MOUSE
Q5F2IO_MOUSE
KV5A_MOUSE
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GGGMXB HUMAN

KV3M HUMAN

GGGMV9 HUMAN

GGGMW0 HUMAN

GG FILB HUMAN

GF FILB HUMAN

GP FILB HUMAN

GO POSES

KV3F HUMAN
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KV5P_MOUSE
Q9UL70_HUMAN
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Q58EŪ8 MOUSE
                     GenCore version (c) 1993 - 2006
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KV1Y HUMAN
KV3H MOUSE
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Maximum Match 100%
Listing first 45 summaries
                                                                                                           protein search, using sw model
                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                 US-09-889-936A-8
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Match Length
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Balb/c;
PubMed=15465827; DOI=10.1074/jbc.M407213200;
Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
Briand J.P., Hoebeke J.;
"Modulation of the Mz muscarinic acetylcholine receptor activity with modulation activity activity with J. Biol. Chem. 279:55697-55706(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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0894j0
065gmw1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.6%; Score 531; DB 2;
91.2%; Pred. No. 2.4e-48;
                                                                                                                                                                                                                                                                                                                   05-001, integrated into UniProtKB/TrEMBL. 05-001.2004, sequence version 1. 07-PEB-2006, entry version 11. Screw BBES protein (Fragment). Name=scPv BBES;
                                                                                                                                                                                                                                                                                            255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ746180; CAG34081.1; -; Other_DNA.
HSSP; P01837; IKCR.
InterPro; IPR01559; Ig.
InterPro; IPR01510; Ig-like.
InterPro; IPR031306; V-Get.
SWART; SW00409; IG; 2.
FROSITE; PSS0835; IG LIKE; 2.
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                   Q66JS7 MOUSE
Q8NEKO_HUMAN
                                                                                                                                                                                                                        ALIGNMENTS
                                                    Q7Z3Y4 HUMAN
KV2G MÕUSE
Q9UL79 HUMAN
Q9UL83 HUMAN
                                                                                               Q9UL83_HUMAN
KV3M_MÕUSE
KV3I_MOUSE
                                         2652C0 MOUSE
                                                                                                                                                                KV1V HÜMAN
Q9UL85 HUMAN
                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                            PRELIMINARY;
    40000100110010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 103; Conservative
  1115
1236
2236
2236
1113
1131
1231
1239
108
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 NCBI_TaxID=10090;
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KV4A HUMAN
P01625;
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                                                                                                                               NEDLINE-22388257; PubMed=12477922; DOI=10.1073/pnas.242603899;
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A batchenko, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carainci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toobhlyuki S., Carainci P., Prange C.,
A Brownstein M.J., Worley W.C., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley W., Sodergren E.J., Lu X., Gibbs R.A.,
A Rahey J., Helton B., Ketreman M., Madan A., Rodrigues S., Sanchez A.,
Bhiting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,
Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smallus D.E.,
Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smallus D.E.,
Bromerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Brownerch A., Schein J.E., Jones W.A.,
Brownerch A., Schein J.E., Jones W.A.,
Brownerch A., Schein J.E., Jones M.A.,
Brownerch A., Schein J.E., Jones W.A.,
Brownerch A., Schein J.E., Jones M.A.,
Brownerch A., Sche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 GDIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSYNQKNYLAWYQQKPGQSPKLLIYWAST
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                  [1]
NUCLEOTIDE SEQUENCE.
STRAIN=Mix FVB/N; TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months
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STRAIN-Mix FVB/N; TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH MGC Project; Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein. SEQUENCE 240 AA; 26609 MW; CF8630CCC002E52C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                             24-MAY-2005, integrated into UniProtKB/TrEMBL
                             240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BC094049; AAH44049.1; -; mRNA.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig.MC.
InterPro; IPR003596; Ig.MC.
InterPro; IPR003596; Ig. V.
Ffam; PF07654; CI-8et; I.
SWART; SW00409; IG.1.
SWART; SW00409; IG.1.
PROSITE; PS00290; IG LIKE; 2.
PROSITE; PS00290; IG LIKE; 2.
                             PRT;
                                                                                                     24-MAY-2005, sequence version 1.
07-FBB-2006, entry version 10.
Hypothetical protein.
Mus musculus (Mouse).
                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90; Conservative
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                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                             Q52L64_MOUSE
052164 MOUSE
11D 052164 MOUSE
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=76004342; PubMed=50995; Schneider M., Hilschmann N.; Schneider M., Hilschmann N.; The primary structure of a monoclonic immunoglobulin-L-chain of subgroup IV of the kappe type (Bence-Jones protein Len)."; Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
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PROSITE; PS50835; IG LIKE; 1.
BROSITE; Bence-Jones protein; Direct protein sequencing;
Immunoglobulin domain; Immunoglobulin V region.
CHAIN 1 >114 /FTId=PRO_0000059768.

FTID=PRO_0000059768.

FTID=PRO_0000059768.
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                                  21.-UUL-1986, integrated into UnibrotKB/Swiss-Prot. 01-OCT-1996, sequence version 2. 07-MAR-2006, entry version 50. Ig kappa chain V-IV region Len.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDB; IEEQ; X-ray; A/B=1-114.
PDB; IEEQ; X-ray; A/B=1-114.
PDB; IEEQ; X-ray; A=1-114.
PDB; IEKG; X-ray; A=1-114.
PDB; ILVE; X-ray; 0=1-114.
PDB; ZLVE; X-ray; 0=1-114.
PDB; ZLVE; X-ray; 0=1-114.
PDB; ALVE; X-ray; 0=1-114.
PDB; ALVE; X-ray; 0=1-114.
PDB; SLVE; X-ray; A=1-114.
PDB; GO: 000383; F: antigen binding; NAS.
GO; GO: 0000582; F: antigen binding; NAS.
GO; GO: 0000595; P: immune response; NAS.
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InterPro; IPR00110; Ig-like.
InterPro; IPR001306; Ig-v.
InterPro; IPR013106; V-set.
SMART; SM00409; IG-1.
SMART; SM00406; IGv; I.
STANDARD;
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NCBI_TaxID=9606;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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MEDLINE=86041854; PubMed=2997713;
Marsh P., Mills F., Gould H.;
"Detection of a unique human V kappa IV germline gene by a cloned cDNA
                                                                                                                                                                                                                                                                                                                                                                                            DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
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Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                          12640 MW; 0647F1D17F236485 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1988, integrated into UniProtKB/Swiss-Prot. 01-APR-1988, sequence version 1. 07-WAR-2006, entry version 45. Ig kappa chain V-IV region B17 precursor.
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SMR; PO6314; 21-134.
LinkHub; PO6314; 21-134.
GO; GO:0005376; C:extracellular region; NAS.
GO; GO:000535; P:imumine response; NAS.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR013106; Veet.
InterPro; IPR013106; Veet.
FORMER; SM00409; IG; 1.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE (GENOMIC DNA).
MEDLINE-86041853; PubMed-2997712;
Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Subgroup IV of human immunoglobulin K light chains is encoded by
                                                                                     Ig kappa chain V-IV region Bl7.
/FTId=PRO_000015183.
Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                       / Match 74.9%; Score 454; DB 1; Length 134; Local Similarity 75.4%; Pred. No. 2.1e-40; nes 86; Conservative 13; Mismatches 15; Indels
                                                                                                                                                     Complementarity-determining-1. Framework-2.
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Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                          14966 MW; 6413A22FD0738832 CRC64;
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PIR; A01904; K4HUJ1.
HSSP; P01625; LIVE.
SMR; P06313; 21-133.
GO; GO:0003576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006555; P:immune response; NAS.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
SMART; SM00406; IG.
SMART; SM00406; IG?; I.
SMART; SM00406; IG?; I.
SMART; SM00406; IG; I.
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NCBI_TaxID=10090;
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                                                                                                                                                                  20 GDIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAMYQQKPGQPPKLLIYWAST
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
                                                                                                                                                                                              63 RDSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                                                                                       "Subgroup IV of human immunoglobulin K light chains is encoded by a
                                                                                                                                    7;
                                                                                                                ; Score 452.5; DB 1; Length 133;
; Pred. No. 3e-40;
10; Mismatches 15; Indels 1.
                   Complementarity-determining-1.
                                      Complementarity-determining-2.
                                                          Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                     sind e germline gene.";
Nucleic Acids Res. 13:6515-6529(1985).
-!- MISCELLANEOUS: There is only one Ig kappa V-IV gene.
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                                                                                               14633 MW; SFB3953066744AF4 CRC64;
                                                                                                                                                                                                                                                                               01-JAN-1988, integrated into UniProtXB/Swiss-Prot.
 /FTId=PRO_0000015182
Framework-1.
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07-MAR-2006, entry version 45.
Ig kappa chain V-IV region precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 200023; CAA77318.1; -; Genomic_DNA.
PIR; A01902; K4HU.
HSSP; P01625; ILVE.
SMR; P06312; 12-121.
Ensembl; ENSG0000153586; Homo sapiens.
HGNC; HGNC:5834; IGKV4-1.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0005825; F:antigen binding; NAS.
GO; GO:0005955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007396; Ig-.
InterPro; IPR003396; Ig-.
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                               Framework-2
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SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                  74.78;
                                                                                                                           Local Similarity 77.2
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Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                       Gaps
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MEDLINE=62059477; PubMed=6170937;
Hamlyn P.H., Gait M.J., Milstein C.;
Complete sequence of an immunoglobulin mRNA using specific priming and the dideoxynucleotide method of RNA sequencing.";
Nucleic Acids Res. 9:4485-4494(1981).
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Svasti J., Milstein C.;
The complete amino acid sequence of a mouse kappa light chain.";
Blochem. J. 128:427-444(1972).
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InterPro; IPR003599; Ig.
InterPro; IPR013106; Ug-like.
InterPro; IPR013106; V-Set.
Pfam; PF07686; V-Set.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
3D-SITTE; PS50835; IG_LIKE; 1.
3D-SITTE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
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/FTId=PRO 0000015190.
Framework-1.
                 Complementarity-determining-1. 
Framework-2.
                                                                                                             Complementarity-determining-3. By similarity.
                                                                                                                                                                                                                                            Length 121;
                                                                  Complementarity-determining-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  13380 MW; 9586AD4188D33974 CRC64;
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                                                                                                                                                                                                                                       67.7%; Score 410; DB 1;
76.5%; Pred. No. 9.6e-36;
iive 10; Mismatches 14;
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PDB; 11GC; X-ray; L=30-136.
Ensembl; ENSMUSG0000060300; Mus musculus.
LinkHub; P01634; --
                                                                                             Framework-3.
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                                                                                                                                                                                                                                                                  Local Similarity 76.59
Tes 78; Conservative
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                                                                                                                                                                                           121 AA;
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Ensembl; ENSMUSG0000052500; Mus musculus.
InterPro; IPR013106; V-set.
Pfam; PR07666; V-set; 1.
SWART; SW00409; IG; 1.
SWART; SM00406; IGv; 1.
PROSITE; PSS0835; IG_LIKE; 1.
Direct protein sequencing; Im
Imwunoglobulin V region.
CHAIN
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                                                                                                                                                       109 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                  Homo Sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                   3 GDIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFI
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                 63 RDSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                                                                                                                                                                                         TISSUB=Abdominal adipose tissue,
MEDLINE=98249779; PubMed=9588180; DOI=10.1006/bbrc.1998.8515;
Olsen K.E., Sletten K., Westermark P.;
Extended analysis of AL-amyloid protein from abdominal wall subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
Biochem. Biophys. Res. Commun. 245:713-716(1998).
                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                   66.3%; Score 402; DB 1; Length 136; 67.5%; Pred. No. 8e-35;
        Complementarity-determining-2.
                Framework-3.
Complementarity-determining-3.
                                                                                                                                                                                                                                                    15; Indels
                                                                                                                                                                                                                      14902 MW; 8CDD85113996D1C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                            P83593;
30-MAY-2003, integrated into UniProtKB/Swiss-Prot.
30-MAY-2003, sequence version 1.
07-MAR-2006, entry version 23.
Ig kappa chain V-IV region STH (Fragment).
                                                                                                                                                                                                                                                                                                                                                      109 AA
                                                                                                                                                                                                                                                    16; Mismatches
                                 Framework-4.
  Framework-2
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InterPro, IPR003599; Ig.
InterPro, IPR007110; Ig-like.
InterPro, IPR003596; Ig_v.
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Best Local Similarity 67.59
Matches 77; Conservative
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 136 AA;
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Distributed under the Creative Commons Attribution-NoDerivs License
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MEDLINE=89035545; PubMed=3141511;
Claflin J.L., Berry J.;
"Genetics of the phosphocholine-specific antibody response to
Streptococcus pneumoniae. Germ-line but not mutated T15 antibodies are
dominantly selected.";
J. Immunol. 141:4012-4019(1988).
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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MEDINE=81241357; PubMed=6788890; DOI=10.1084/jem.153.5.1366;
MEDINE=81241357; PubMed=6788890; JOI Leder P., Scharff M.D.;
"Kwan S.-P., Rudikoff S., Seidman J.G., Leder P., Scharff M.D.;
"Nucleic acid and protein sequences of phosphocholine-binding light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTK 112
                                                                            Ig kappa chain V-IV region STH.
/FIId=PRO_000059769.
Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 109;
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1.
Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.2%; Score 401; DB 1; 70.6%; Pred. No. 7.8e-35;
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                                                                                                                                                                                                                                                               Framework-3.
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PIR; A01915; KVMS7A.
HSSP; Q9ERZ9; ZAP2.
SMR; P01632; 1-114.
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Best Local Similarity 70.6%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-22716456; PubMed=12833571; DOI=10.1002/jmr.617; Brlandsson A., Holm P., Ullen A., Stigbrand T., Sundstrom B.E.; "Studies of the interactions between the anticytokeratin 8 monoclonal antibody TS1, its antigen and its anti-idiotypic antibody alphaf51."; J. Mol. Recognit. 16:157-163(2003)
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
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                                                                                                                                                                                        Ig kappa chain V-I region S107A. /FIId=PRO 0000059770. Pramework-I.
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                                                                                                                                                                                                                                                                                                                                                                                                              12717 MW; 32008EC8E9DBE67B CRC64;
          InterPro; IPR001599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR001106; V-8et.
InterPro; IPR01106; V-8et.
Pfam; PF07686; V-eet; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGV; 1.
INTERPROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region.
CHAIN
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InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
InterPro; IPR013106; V-Set.
SMART; SM00409; IG; I.
PROSITE; PS50835; IG_LIKE; I.
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OSF210;
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MGI:3577282; U29423
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Distributed under the Creative Commons Attribution-NoDerivs License
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Biochem. J. 171:337-347(1978).
Biochem. J. 171:337-347(1978).
-!- MISCELLANGOUS: The mature chain has 12 additional residues at its amino end, due to a tandem duplication of 36 nucleotides after the codon for residue 36. Residue 42 corresponds to the N-terminal residue of typical kappa chains.
                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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MEDLINE=83001944; PubMed=6288267; DOI=10.1016/0092-8674(82)90184-2;
Kelley D.E., Coleclough C., Perry R.P.;
"Functional significance and evolutionary development of the 5'-
terminal regions of immunoglobulin variable-region genes.";
Cell 29:681-689(1982).
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MEDLINES-00176554; PubMed=6245773;
Rabbitcs T.H., Hanlyn P.H., Matthyssens G., Roe B.A.;
"The variability, arrangement, and rearrangement of immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Sequence of the full-length immunoglobulin kappa-chain of mouse
                                                                                                                                                                                                           .;
%
                                                                                                                                              Length 115;
                                                                                                                                                                                                           20; Indels
                                                                                        12560 MW; E4D3BF3D63E88007 CRC64;
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                                                                                                                                              Score 391; DB 2;
Pred. No. 9.9e-34;
                                                                                                                                                                                                        14; Mismatches
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SMSP; PO1634; IIGC.
SMR; PO1633; 42-149.
Ensembl; ENSMUSG0000061362; Mus musculus.
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Can. J. Biochem. 58:176-187(1980)
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MEDLINE=78186617; PubMed=418775;
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InterPro; IPR00710; IG-like.
InterPro; IPR003596; IG.
InterPro; IPR013106; V-Set.
Pfan; PF07686; V-Set.;
SMART; SW00409; IG; 1.
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                                                                                                                                                     64.5%;
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                                                            115
Immunoglobulin domain
                                                                                        115 AA;
                                                                                                                                                                                Similarity
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PIR, S34096; S34096
HSSP; P01625; 1EK3.
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D30607;
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                                                                                                                                                                                                             3 GDIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFI 62
                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000, sequence version 1.
07-FEB-2006, entry version 22.
Myosin-reactive immunoglobulin light chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                        MEDLINE=93170387; PubMed=8436174; Wagner S.D., Luzzatto L.; "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                   RDSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                                                                                                                                                95 RYIGVPDRFTGSGSGTDFTFTISSVQAEDLAVYYCQQHYSTPPTFGGGTKLEIK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
MEDLINE-92228746; PubMed=1373487;
Sebedee S.L., Barbas C.F. 3rd, Hom Y.L., Caothien R.H., Graff R., DeGraw J., Pyati J., LaPolla R., Burton D.R., Lerner R.A.; "Human combinatorial antibody libraries to hepatitis B surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            foung D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                              Ig kappa chain V-V region MPC11.
/FTId=PRO_000015189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
MEDLINE=92202880; PubMed=1552291; DOI=10.1084/jem.175.4.983;
Martin T., Duffy S.F., Carson D.A., Kipps T.J.;
Exidence for somatic selection of natural autoantibodies.";
J. Exp. Med. 175:983-991(1992).
                                                                     Framework-1.
Complementarity-determining-1.
                                                                                                                                                                       DB 1; Length 149;
                                                                                                 Complementarity-determining-2.
                                                                                                                     Complementarity-determining-3
                                                                                                                                                                                         20; Indels
                                                                                                                                                   16434 MW; B0480C87B682AC3E CRC64;
protein sequencing; Immunoglobulin domain; globulin V region; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 89:3175-3179(1992)
                                                                                                                                                                     63.5%; Score 385; DB 1; 66.7%; Pred. No. 6e-33; ive 12; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                                                                                                                                                                                                                                                  01-MAY-2000, integrated into UniProtKB/TrEMBL 01-MAY-2000, sequence vorcia-
                                                                                                                                                                                                                                                                                                                          109 AA
                                                                                                                                 Framework-4.
                                                                                         Framework-2
                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           somatic mutation.";
Bur. J. Immunol. 23:391-397(1993)
                                                                                                                                                                                                                                                                                                                          Q9UL78_HUMAN PRELIMINARY;
                                                                                                                                                            Query Match
Best Local Similarity
Local Similarity
Local 76; Conservative
                                              Homo sapiens (Human).
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 Direct protein se
Immunoglobulin V
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                     30
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NON TER
SEQUENCE
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSS----YLAWYQQKPGQAPRLLIYGASSR
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MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
"Autoantibody-associated kappa light chain variable region gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 AA; 11646 MW; SF675C52EC7EE197 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KV3L_HUMAN STANDARD; PRT; 129 AA. P18135; 01-NOV-1990, integrated into UniProtKB/Swiss-Prot. 01-NOV-1990, sequence version 1. 07-MAR.2006, entry version 41. Ig kappa chain V-III region HAH precursor. Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.1%; Score 382.5; DB 2
64.6%; Pred. No. 7.6e-33;
iive 17; Mismatches 18
                                                                                EMBL; AF035036; AAD56272.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
InterPro; IPR013106; V-set.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin domain.
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nes 73; Conservative
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SEQUENCE
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                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 GEIVLTQSPGTLSLSPGERATLSCRASQSVSSS-----YLAWYQQKPGQAPRLLIYGASS
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Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
expressed in chronic lymphocytic leukemia with little or no somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 RDSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoantibodies expressed in patients with chronic lymphocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CZECH II; TISSUE-Mammary tumor metastatized to lung.
MMTV-LTR/Wntl model. Expression driven by an MMTV-LTR enhancer.;
MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŝ
                         mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
-1- DISEASE: The protein is one of the surface immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.0%; Score 381.5; DB 1; Length 129; 64.0%; Pred. No. 1.2e-32; ive 17; Mismatches 19; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig kappa chain V-III region HAH.
/FTId=PRO 0000015179.
Framework-1.
                                                                                                                                                                                                                                                                PRR; PL0022; K3HUHA.

RISSP; P01625; IEEQ.

RIK; P18135; 21-129.

Ensembl; ENGGO000169769; Homo sapiens.

LinkHub; P18135; -.

GO; GO:0005576; C:extracellular region; NAS.

GO; GO:0005576; C:extracellular region; NAS.

GO; GO:0005376; P:immune response; NAS.

InterPro; IPR003109; Ig.

InterPro; IPR013106; V-Set.

InterPro; IPR013106; V-Set.

REm; PR07686; V-Set; 1.

SWART; SM00406; IG'; I.

RRART; SM00406; IG'; I.

RROSITE; PSS0835; IG LIKE; 1.

RROSITE; PSS0835; IG LIKE; 1.

RIMMUNOGlobulin domain; Immunoglobulin V region; Signal.

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129
129 AA;
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hasteh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robark S.A., McEwan P.J., McKernan K.J., Malke J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Schein J.M., Mannar M.A.,
Schein J.E., Jones S.J.M., Marra M.A.,
Schein J.E., Jones S.J.M., Marra M.A.,
Schein J.E., Jones S.J.M., Marra M.A.,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SRGDIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGV
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MMTV-LTR/Wntl model. Expression driven by an MMTV-LTR enhancer.;
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07-MAR-2006, entry version 43.
Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 239 AA; Z6302 MW; 98FC4BA8EB404215 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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MGI; MGI:96495; IGK-C.

INTERPRO; IPRO03159; IG.

INTERPRO; IPR003109; IG-11ke.

INTERPRO; IPR0031006; IG-MHC.

INTERPRO; IPR0031006; IG-N.

INTERPRO; IPR013106; V-GET.

Pfam; PP07654; C1-8et; 1.

SMART; SM00407; IG-1; 1.

SMART; SM00407; IG-1; 1.
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                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 GEIVWITGSPATLSVSPGERATLSCRASQSVSNN-----LAWYQQKPGQPPRLLIYGAST
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NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=8617570; PubMed=3063417;
Jurik F.R., Sorge J., Frog S., Heitzmann J.G., Curd J.G., Chen P.P.,
Goldfien R., Carson D.A.;
"Cloning and sequence determination of a human rheumatoid factor
light-chain gene."

light-Anal gene."

Proc. Natl. Acad. Sci. U.S. A. 83:2195-2199(1986).
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Framework-1.
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MSR; PO1625; 1LVE.

MSR; PO4207; -1.29.

LinkHub; PO4207; -..

GO; GO:0005576; C:extracellular region; NAS.

GO; GO:0005823; F:antigen binding; NAS.

GO; GO:0005959; P:immune response; NAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR007110; Ig-like.

InterPro; IPR013106; V-set.

Pfam; PF07686; V-set; 1...

SNART; SM00409; IG; 1...

SNART; SM00406; IGv; 1...

MRNSITE; PS50835; IG_LIKE; 1...
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Search completed: May 19, 2006, 17:46:32 Job time : 178.762 secs

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: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:*
: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:*
: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:*
: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:*
: /EMC Celerra SIDS3/ptodata/2/iaa/PGTUS COMB.pep:*
: /EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-08-470-110A-45
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US-08-107-659D-2
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US-09-102-753A-4
US-09-657-274-4
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US-09-657-274-4
US-09-657-769A-46
US-08-667-769A-46
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        US-09-232-290-26
        Sequence 16, Appl 20

        29
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        US-00-667-769A-16
        Sequence 16, Appl 30

        30
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        US-09-509-17082A-16
        Sequence 16, Appl 31

        31
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        Sequence 16, Appl 32

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        US-09-509-17082A-17
        Sequence 16, Appl 34

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        US-09-564-47
        Sequence 47, Appl 34

        35
        518
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        US-09-561-100-9
        Sequence 9, Appl 36

        36
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        Sequence 9, Appl 36

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        Sequence 9, Appl 36

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RESULT I
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Sequence 45. Application US/08467420A
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SPELICANT: Ames, Robert S.
APPLICANT: Chaiden, Irvain M.
APPLICANT: Chaiden, Irvain M.
APPLICANT: Graden, Irvain M.
APPLICANT: Graden, Irvain M.
APPLICANT: Holmes, Stephan D.
APPLICANT: Holmes, Stephan D.
APPLICANT: Theiser, Theiser, Train M.
APPLICANT: Theiser, Theiser, Theorety
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 74
CORRESPONDENCE: ADDRESS:
ADDRESSEE: Intellectual Property
CORRESPONDENCE: ADDRESS:
ADDRESSEE: Intellectual Property
CORRESPONDENCE: ADDRESS:
ADDRESSEE: Mitchline Beecham Corp./Corporate
ADDRESSEE: Mitchline Becham Corp./Corporate
ADDRESSEE: Mitchline FORM:
CORPUTER: IPO OF MISSES
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CORPUTER: IBN PC Compatible
COMPUTER: IBN PC COMPATION:
APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE:
CLASSIFICATION NUMBER: P50282
TELECOMMUNICATION INFORMATION:
AREFERRACE ADDRESSES
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1 BLYWIQSPSSLSVSAGGEKVIMSCKSSQSLLNSGNQKNYLAWYQQKPGQPPKLLIYGASTR 60
                                                      64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 91.2
Matches 103; Conservative
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                                                                                                                                                           US-08-667-769A-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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                                                                                                                            63
                                                                                                                                              1 ELVMIQSPSSLSVSAGEKVTMSCKSSQSLLNSGNQKNYLAWYQQKPGQPPKLLIYGASTR 60
                                                                                                                          4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                             64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
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                                                      Query Match 89.3%; Score 541; DB 1; Length 113; Best Local Similarity 91.2%; Pred. No. 2.2e-42; Matches 103; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
89.3%; Score 541; DB 1; Length 113;
Sest Local Similarity 91.2%; Pred. No. 2.2e-42;
Matches 103; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,110A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: 950282
TELECOMMUNICATION INFORMATION: TELEPHONE: 610 270-5024
TELEFAX: 610 270-5020
INFORMATION FOR SEQ ID NO: 45:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
   ; MOLECULE TYPE: protein US-08-467-420A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: eir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                    US-08-470-110A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-470-110A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                  RESULT 2
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                                                                                                                                           APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Treatment of IL5 Antagonists Useful in
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.3%; Score 541; DB 1; Length 113; 91.2%; Pred. No. 2.2e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: RADAPY disk
MEDIUM TYPE: RADAPY disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
SOGTWARE: Patentin Release #1.0, Version #1.30
SOGTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/67,769A
FILING DATE: 22-DEC-1995
PRIOR APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
RRIOR APPLICATION NUMBER: US 08/467420
FILING DATE: 06-JUN-1995
RRIOR APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATORNEY AGENT INFORMATION:
NUMBE: SULECTION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATORNEY AGENT INFORMATION:
NUMBE: SULECTION, JUMBER: US 08/363131
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEE: SmithKline Beecham Corp./Corporate: P.O. Box 1539-UW2220
King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
Sequence 45, Application US/08667769A, Patent No. 5783184, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: P50503
                                                                                              Ames, Robert S.
Appelbaum, Edward R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028
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ELVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSGNQKNYLAWYQQKPGQPPKLL1YGASTR 60
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                                                                 64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
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                                                                                                                                                                                                   Sequence 45, Application US/08940371
Patent No. 5851525
GENERAL INPORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Chalken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
ITILE OF INVENTION: Recombinant IL5 Antagonists Useful in ITILE OF INVENTION: Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.3%; Score 541; DB 1; Length 113;
91.2%; Pred. No. 2.2e-42;
tive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19406-0939

ZIP: 19406-0939

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P. O. Box 1539-UW2220 CITY: King of Prussia STATE: Pennsylvania COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/470,110
FILING DATE:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: SULTON, JEFFERY A.
REGISTRATION NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: P50282
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 610 270-5090
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
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Best Local Similarity 91.2
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                            APPLICANT Ames, Robert S.
APPLICANT Ames, Robert S.
APPLICANT Chaiken, Irwin M.
APPLICANT Chaiken, Irwin M.
APPLICANT Cook, Richard M.
APPLICANT Cook, Mitchell S.
APPLICANT Gross, Mitchell S.
APPLICANT Theisen, Timothy W.
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property
STREET: P. O. Box 1539-UW220
CITY: King of Prussia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 541; DB 2; Length 113;
Pred. No. 2.2e-42;
4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    STALL.
COUNTRY: USA
ZUP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/637,647
FILING DATE: 19-JUN-1997
FILING DATE: 19-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 %30-10-700-740-45

%Sequence 45, Application US/10700740

; Patent No. 6946130

; GENERAL INFORMATION:

; APPLICANT: Ames, Robert S.
Sequence 45, Application US/08637647 Patent No. 6129913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5024
TELEPAX: 610 270-5090
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 89.3%;
Best Local Similarity 91.2%;
Matches 103; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-17082A-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
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Appelbaum, Edward R.
Chaiken, Irwin M.
Cook, Richard M.
Gross, Mitchell S.
Holmes, Stephen D.
McMillan, Lynette J.
Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
Treatment of IL5 Mediated Disorders
                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 76

CORRESPONDENCES: 76

CORRESPONDENCES: 76

CONTRY: King of Prussia

STATE: Pennsylvania

CITY: King of Prussia

CONTRY: USA

ZIP: 19406-0939

COMPUTER: EDAN PC Compatible

OCOMPUTER: IBM PC COMPATIBLE

OCOMPUTER: INFORMATION:

OCOMPUTER: INFORMATION:

OCOMPUTER: OCOMPATION:

OCOMPUTER: INFORMATION:

OCOMPUTER: INFOR
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89.3%; Score 541; DB 2;
Best Local Similarity 91.2%; Pred. No. 2.2e-42;
Matches 103; Conservative 4; Mismatches 6
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TOPOLOGY: linear
MOLECTUE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-700-740-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 45, Application PC/TUS9517082A
GENERAL INFORMATION:
APPLICANT: Amee, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chalken, Irwin M.
APPLICANT: Cook, Richard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US95-17082A-45
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y APPLICANT: Gras, Airchell S.

APPLICANT: Holmas, Stephen D.

APPLICANT: Holmas, Stephen D.

APPLICANT: Holmas, Are Medillan, Underte J.

APPLICANT: Holmas, Timothy W.

COMBESSER: Gmithkine Beecham Corp./Corporate

STREET: P. O. Bet 1339-WA2200

CITY, King of Prussia

COMPUTES: Him Proceed W.

COMPUTES: Him Proceed W.

COMPUTES: Him Proceed W.

COMPUTES: Timothy W.

COMPUTES: Him Proceed W.

COMPUTES: Him Proceed W.

COMPUTES: Him Proceed W.

COMPUTES: Him Proceed W.

COMPUTES: Timothy W.

COMPUTES: Petcentr Nelses #1.0, Version #1.30

SOFTAME: Petcentr Nelses #1.0, Version #1.30

COMPUTES: Petcentr Nelses #1.0, Version #1.30

COMPUTES: W. Dec. 1994

COMPUTES: W. Dec. 1995

COMPUTED: W. Dec. 1995

COMPUTES: W. Dec. 1995

COMPUTED: W. Dec. 1995

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= CDR1
/note= "Complementarity Determining
Region 1 (CDR1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= CDR2
/note= "Complementarity Determining
Region 2 (CDR2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Monoclonal antibody McPC603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Light chain variable region (V-L)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Framework Region 1 (FR1)"
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/note= "Framework Region 2 (FR2)"
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                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SEGURAR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,252B
FILING DATE: 14-JUN-1993
CLASSIFICATION NUMBER: US/08/077,252B
REGISTRATION NUMBER: 32,762
REFERENCE/POCKET NUMBER: 15280-152
REFERENCE/POCKET NUMBER: 15280-152
RELEPHONE: (415) 576-0300
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
TELEFORM CHARACTERISTICS:
TELEFORM CHARACTERISTICS:
TELEFORM CHARACTERISTICS:
TYBE: amino acid
                                                                       : Two Embarcadero Center, Eighth Floor
San Francisco
California
Y: USA
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= FR3
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NAME/KEY: Modified-site
LOCATION: 49
OTHER INFORMATION:
OTHER INFORMATION: residuc
OTHER INFORMATION: paired
OTHER INFORMATION: position
OTHER INFORMATION: for pc
OTHER INFORMATION: disulf
FEATURE:
NAME/KEY: Region
LOCATION: 56.62
OTHER INFORMATION: /labe
OTHER INFORMATION: /note
OTHER INFORMATION: /note
OTHER INFORMATION: /note
OTHER INFORMATION: /note
FEATURE:
FEATURE
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NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
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LOCATION: 41..55
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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LOCATION: 1..113
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 1..23
OTHER INFORMATION:
OTHER INFORMATION:
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NAMEJ/KEY:
REGION
LOCATION:
24.40
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 63..94
OTHER INFORMATION:
OTHER INFORMATION:
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1 DIVMTQSPSSLSVSAGERVTMSCKSSQSLLNSGNQKNFLAWYQQKPGQPPKLLIYGASTR
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Patent No. 5766886
GENERAL INFORMATION:
APPLICANT: Studincka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Light chain variable region Ala residue that can be changed to Cys, paired with Heavy chain variable region 1905tion 144 Arg residue change to Cys, for possible 31 site interchain disulfide bond"
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ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 2006-3934
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,669D
FILING DATE: 13-AUG-1993
CLASSIFICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
RRIOR APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US/08/08/04
FILING DATE: 13-DEC-1991
ATORNEY/AGBNT INFORMATION:
NAME: Michele A. Cimbala
                          /note= "V-L93 Ser to Tyr mutation site (pseudo-symmetrically related to V-H97 Ser to Tyr mutation site in Heavy chain variable region)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 113;
                                                                                                                                                                                                           /label= CDR3
/note= "Complementarity Determining
Region 3 (CDR3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 88.4%; Score 536; DB 1; Length 11 Best Local Similarity 91.2%; Pred. No. 6.3e-42; Matches 103; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                         LOCATION: 104..109
OTHER INFORMATION: /label= FR4
OTHER INFORMATION: /note= "Framework Region 4 (FR4)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Modified-site
LOCATION: 93
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
NAME/KEY: Region
LOCATION:
OTHER INFORMATION:
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NAME/KEY: Region
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Query Match
Best Local Similarity
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US-08-477-531B-2
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                                                                                                                                                                                                                               Score 536; DB 1; Length 113;
Pred. No. 6.3e-42;
3; Mismatches 7; Indels
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Patent No. 5770196
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,788A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US/082,842
PRIOR APPLICATION NUMBER: US/082,842
PRIOR APPLICATION NUMBER: 23-JUN-1993
PRIOR APPLICATION NUMBER: US/082/10906
FILING DATE: 13-JUN-1992
PRIOR APPLICATION NUMBER: US/07/808,464
FILING DATE: 13-DEC-1992
PRIOR APPLICATION NUMBER: US/07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REGISTRATION NUMBER: 33,851
REGISTRATION NUMBER: 33,851
REGISTRATION NUMBER: 33,851
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: 202/371-2540
     0610.1000001/MAC
                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Query Match
Best Local Similarity 91.2%;
Matches 103; Conservative
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amino acid
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                                                                                                                                                                      MOLECULE TYPE: protein US-08-107-669D-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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US-08-472-788A-2
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                                                                                                                                     1 DIVMTQSPSSLSVSAGERVTMSCKSSQSLLNSGNQKNPLAWYQQKPGQPPKLLIYGASTR
                                                                                                          4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
ATTLE OF INVENTION:
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSES: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                             64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
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Length 113;
88.4%; Score 536; DB 1; Length 11
91.2%; Pred. No. 6.3e-42;
ive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington STATE: D.C.
COUTRY: United States of America
COUNTRY: United States of America
ZIP: ZOO05-3334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PerentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,531B
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 436

REIGRATION DATA:
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
PRIOR APPLICATION NUMBER: 08/107,669
FILING DATE: 14-DEC-1992
PRIOR APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR RAPLICATION DATA: APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. CIMBAIA
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610:1000004/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER: US/08/477,531B
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08477531B Patent No. 5821123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 113 amino acids TYPE: amino acid
                                                      Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
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/label= CDR1
/note= "Complementarity Determining
Region 1 (CDR1)"
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/note= "Complementarity Determining
Region 2 (CDR2)"
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/note= "Complementarity Determining
Region 3 (CDR3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Monoclonal antibody McPC603
Light chain variable region (V-L)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= FR2
/note= "Framework Region 2 (FR2)"
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/note= "Framework Region 1 (FR1)"
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                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Blopy disk
COMPUTER: IBM PC compatible
CLASSIFICATION NUMBER: US 08/077,252
FILING DATE: 14-JUN-1993
ATTORNEY/AGENT INPORMATION:
NAME: Weber, Ellen Lauver
REFERENCE/DOCKET NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 32,762
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAME (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUIENCE CHARACTERISTICS:
COMPUTER: CALSACTERISTICS:
COMPUTER: ACCOUNT 
             SSEE: Townsend and Townsend and Crew LLP

: Two Embarcadero Center, Eighth Floor

San Francisco

California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= FR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAMEA/KEY: REGION
LOCATION: 1.23
OTHER INFORMATION:
OTHER INFORMATION:
FATURE:
NAME/KEY: REGION
LOCATION: 24.40
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FATURE:
FATURE:
LOCATION: 41.55
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
PEATURE:
NAME/KEY: Region
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LOCATION: 95. 103
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Region
                                                                                                                                                        COUNTRY:
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Sequence 4, Application US/09002753A

Parent No. 6147203

GENERAL INFORMATION:
APPLICANT: Bestan, Ira
APPLICANT: Lee, Byungkook
APPLICANT: Jung, Sun-Hee
APPLICANT: Berinkmann, Ulrich
TITLE OF INVENTION: Recombinant Disulfide-Stabilized
TITLE OF INVENTION: Polypeptide Fragments Having Binding Specificity
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                         Sequence 2, Application US/08082842A
| Patent No. 5869619
| GENERAL INFORMATION:
| APPLICANT: Studnicka, Gary M.
| TILLE OF INVENTION: Modified Antibody Variable Domains
| NUMBER OF SEQUENCES: 89
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
| STREET: 1100 New York Ave., N.W., Suite 600
| CITY: Weshington
| STRIET: D.C.
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.4%; Score 536; DB 1; Length 113; 91.2%; Pred. No. 6.3e-42; Live 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTE: USA

ZIP: COUNTRY: USA

ZIP: 2005-3934

COMPUTER: ELOPPY disk

COMPUTER: ELOPPY disk

COMPUTER: END FC compatible

COMPUTER: IBM FC compatible

COMPUTER: DatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/082,842A

FILING DATE: 23-JUN-1993

CLASSIFICATION: DATA:

APPLICATION NUMBER: PCT/US92/10906

FILING DATE: 14-DEC-1992

PRILOM APPLICATION DATA:

APPLICATION NUMBER: US 07/808,464

FILING DATE: 13-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Cimbala, Michele A.

REFERENCE/DOCKET NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 0610:1000002

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 113 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 103; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                     US-08-082-842A-2
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                                                        RESULT 12
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APPLICANT:
APPLICANT:
TITLE OF INVENTION: Recombinant Disulfide-Stabilized
TITLE OF INVENTION: Polypeptide Fragments Having Binding Specificity
NUMBER OF SEQUENCES: 14
COMPUTER READALE FORM:
COMPUTER: PLORDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06687
FILING DATE: 14-JUN-1994
CLASSIFICATION:
ATTORNEY/AGENT INPRMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REGISTRATION NUMBER: 15.280-15.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRONE: (415) 543-5643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIVWIQSPSSLSVSAGERVIMSCKSSQSLLNSGNQKNFLAWYQQKPGQPPKLLIYGASTR
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                                                                                              /note= "Complementarity Determining Region 1 (CDR1)"
                                                                                                                                                                                                                                                                                       NAME/KEY: Region
LOCATION: 56.62
OTHER INFORMATION: /label= CDR2
//note= "Complementarity Determining
Region 2 (CDR2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Region
LOCATION: 95..103
OTHER INFORMATION: /label= CDR3
/note= "Complementarity Determining
Region 3 (CDR3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Region
LOCATION: 104.109
OTHER INFORMATION: /label= FR4
OTHER "Framework Region 4 (FR4)"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                  NAME/KEY: Region
LOCATION: 41..55
LOCATION: 41..55
/Notes InfoRMATION: /label= FR2
/notes "Framework Region 2 (FR2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Region
LOCATION: 63.94
OTHER INFORMATION: /label= FR3
/note= "Framework Region 3 (FR3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 4, Application PC/TUS9406687; GENERAL INFORMATION:
                      NAME/KEY: Region
LOCATION: 24..40
OTHER INFORMATION:
    FEATURE:
                                                                                                                                                   FEATURE
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PCT-US94-06687-4
                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
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                                                                                                                                                                                                                                                                                                                     64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                                                                                                                                                                                                                              /note= "Monoclonal antibody McPC603
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MEDIUM TYPE: RIOPPY disk
COMPUTER: IN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/657,274
FILING DATE: 07-Sep-2000
CLASSIFICATION NUMBER: 09/002,753
PRIOR APPLICATION NUMBER: 09/002,753
APPLICATION NUMBER: 09/002,753
APPLICATION NUMBER: 09/002,753
TELING DATE: CURROWATION:
NAME: Weber, Ellen Lauver
REFERENCE/DOCKET NUMBER: 32,762
REGISTRATION NUMBER: 32,762
TELEPHONE: (415) 576-0200
                                                                                                                       Length 113;
                                                                                                                                                                       7; Indels
LOCATION: 104..109
OTHER INFORMATION: /label= FR4
OTHER INFORMATION: /note= "Framework Region 4 (FR4)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 23 CORRESSONDERS: 23 CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESSE: Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: Callfornia COUNTRY: USA
                                                                                                                     Query Match

88.4%; Score 536; DB 2;
Best Local Similarity 91.2%; Pred. No. 6.3e-42;
Matches 103; Conservative 3; Mismatches 7.
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/note= "Framework Region 1 (FR1)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09657274
Patent No. 6558672
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1.23
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Pastan, Ira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1.113
OTHER INFORMATION
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US-09-002-753A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Region
LOCATION: 104..113
OTHER INFORMATION: /label= FR4
OTHER INFORMATION: /note= "Framework Region 4"
FEATURE: NAME/KEY: Modified-site
LOCATION: 106
OTHER INFORMATION: to a Cys for possible interchain disulfide bond."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Residue that can be changed to Cys fro possible interchain disulfide bond."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= CDR2
/note= "Complementarity Determining Region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= CDR1
/note= "Complementarity Determining Region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 88.4%; Score 536; DB 5; Length 113; Best Local Similarity 91.2%; Pred. No. 6.3e-42; Matches 103; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) NAME/KEY: Modified-site

) LOCATION: 93

OTHER INFORMATION: /note= "The Ser to Tyr mutation

) OTHER INFORMATION: site."
                                                                                                                                                     NAME/KEY: Region
LOCATION: 1..23
OTHER INFORMATION: /label= FR1
OTHER INFORMATION: /note= "Framework Region 1"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= FR2
/note= "Framework Region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= FR3
/note= "Framework Region 3"
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                          NAME/KE:

LOCATION: 24.40

OTHER INFORMATION: /label-
OTHER INFORMATION: /note=
FATURE:
NAME/KEY: Region
LOCATION: 41.55
OTHER INFORMATION: /note=
FATURE:
NAME/KEY: Modified-site
LOCATION: 49
OTHER INFORMATION: /note=
COTHER INFORMATION: /note=
FATURE:
NAME/KEY: Modified-site
LOCATION: 49
OTHER INFORMATION: /note=
OTHER INFORMATION: /note=
OTHER INFORMATION: /note=
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LOCATION: 56.62
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
NAME/KEY: REGION
LOCATION: 63.94
OTHER INFORMATION:
PEATURE:
NAME/KEY: REGION
LOCATION: 95.103
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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Job time : 34.6032 secs

Search completed: May 19, 2006, 17:48:43

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91, Appl 11, Appl 59, Appl 55, Appl 71, Appl 71, Appl 71, Appl 72, Appl 21, Appl 21, Appl 21, Appl 21, Appl 21, Appl 21, Appl

Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

us-09-889-936a-8.rapbm

OM protein

Run on:

Sequence:

Minimum DB Maximum DB

Database

Result

Searched:

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4 DIVMIQSPSSLSVSAGEKVIMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
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Publication No. US20040091482A9
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Tang, Ying
TITLE OF INVENTION: Related Methods
TITLE OF INVENTION: Related Methods
FILE REFERENCE: PIX 4976
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOUTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Watkins, Jeffry D.
APPLICANT: Huse, William D.
APPLICANT: Tang, Ying
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Related Methods
FILE REFERENCE: P-IX 4976
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 386
SOPTWARE: FastSEQ for Windows Version 4.0
US-10-688-015-71
US-10-688-015-91
US-10-160-505-71
US-11-218-813-71
US-10-238-656-53
US-10-238-656-53
US-10-239-656-53
US-10-700-632-71
US-10-239-656-79
US-10-239-656-69
US-10-239-656-69
US-10-239-656-69
US-10-239-656-69
US-10-239-656-69
US-10-700-632-64
                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09995529 Publication No. US20030099655A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity 92.9
105, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Mus musculus
US-09-995-529-2
      US-09-995-529-2
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US-09-995-529-2
      Query Match
Best Local S:
Matches 105
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Sequence 29, Appl
Sequence 9, Appli
Sequence 9, Appli
Sequence 71, Appl
Sequence 71, Appl
Sequence 71, Appl
Sequence 71, Appl
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45, Appl
2, Appli
2, Appli
2, Appli
68, Appl
46, Appl
16, Appl
16,
                                                                                                                                   May 19, 2006, 17:47:39 ; Search time 114.159 Seconds (without alignments) 470.686 Million cell updates/sec
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Sequence 16,
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Sequence 16,
Sequence 16,
Sequence 16,
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Sequence 45,
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Sequence 2,
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Sequence 46,
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                      GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                             2097797
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US-09-995-529-2

US-10-144-644-45

US-11-076-395-45

US-11-0325-698-2

US-10-345-698-2

US-10-325-688-2

US-10-100-532-68

US-10-700-740-46

US-10-700-740-46

US-10-700-740-46

US-11-076-395-46

US-11-076-395-16

US-11-202-507A-11

US-11-202-507A-11

US-11-202-507A-11

US-11-202-507A-11

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US-11-202-507A-11

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US-10-395-395-18

US-10-395-395-11
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Maximum Match 100%
Listing first 45 summaries
                                                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match 1
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Perfect score:
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Gaps

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Length 113;

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US-10-144-644-45
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                                                                                                                                                                  Gaps
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Publication No. US2003005942941

GENERAL INFORMATION:
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chalken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: McMillan, Lynchell S.
APPLICANT: McMillan, Lynchel S.
APPLICANT: Theisen, Timochy W.
TITLE OF INVENTION: Recombinant ILS Antagoniats Useful in TITLE OF INVENTION: Treatment of ILS Mediated Disorders NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                               Length 113;
                                                                                                               Score 545; DB 3; Length 11
Pred. No. 2.9e-41;
1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATE: US/10/144,644
FILING DATE: 2002-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467420
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION: INFORMATION:
RAGISTRATION NUMBER: 95.028
REFERENCE/DOCKET NUMBER: P50282-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: SmithKline Beecham Corp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: P.O. Box 1539-UW2220
CITY: King of Prussia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION
                                                                                                          89.9%;
Best Local Similarity 92.9%;
Matches 105; Conservative 1
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INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
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                     TYPE: PRT
CORGANISM: Mus musculus
US-09-995-529-2
LENGTH: 113
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                                                                                                    4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
                                                      Gapa
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Score 541; DB 4; Length 113;
Pred. No. 6.6e-41;
4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/700,740
FILING DATE: 04-Nov-2003
CLASSIFICATION: -Unknown>
PRIOR APPLICATION -Unknown>
PRIOR APPLICATION NUMBER: US/10/144,644
FILING DATE: 2002-08-08
APPLICATION NUMBER: US/10/110
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
RADDRESSEE: SMitchKine Beecham Corp
STREET: P.O. Box 1539-UW2220
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P50282-2 TELECOMMUNICATION INFORMATION:
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; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-700-740-45
                                                                                                                                                                                                                                                                                                                                                                       Sequence 45, Application US/10700740; Publication No. US20040156850A1; GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
Appelbaum, Edward R.
Chaiken, Irwin M.
Cook, Richard M.
Gross, Mitchell S.
Holmes, Stephen D.
McMillan, Lymette J.
Thile OF INVENTION: Recombinant IL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 610-270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELEFAX: 610-270-5090
Query Match
Best Local Similarity 91.2%;
Matches 103; Conservative
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SEQUENCE CHARACTERISTICS
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NAME: McNicholas, Janet M. REGISTRATION NUMBER: 32,918
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TELEPHONE: 312/707-8889
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 89.3%;
ilarity 91.2%;
Conservative
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
Query Match
Best Local Similarity
Matches 103; Conserv
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tes 103; Conserv
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                                                                                                4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
                                         Gaps
                                                                                                                                                      64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant IL5 Antagonists Useful in
Treatment of IL5 Mediated Disorders
   Length 113;
89.3%; Score 541; DB 4; Length 11 llarity 91.2%; Pred. No. 6.6e-41; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/076,395
FILING DATE: 09-Mar-2005
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/10/700,740
FILING DATE: 04-00-2003
APPLICATION NUMBER: US/10/14,644
FILING DATE: 2002-08-08
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/46720
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp
STREET: P.O. Box 1539-UW2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Sucton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
INFORMATION FOR SEQ 1D NO: 45:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-11-076-395-45
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ames, Robert S.
Appelbaum, Edward R.
Chaiken, Irwin M.
Cook, Richard M.
Gross, Mitchell S.
Holmes, Stephen D.
McMillan, Lynette J.
Theisen, Timothy W.
TITLE OF INVENTION: Recombinant II
                                                                                                                                                                                                                                                                                      Sequence 45, Application US/11076395
Publication No. US20060029594A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 113 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                   Similarity
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US-11-076-395-45
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Query Match
                                       Matches
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                                                                                       4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLJYGVFIR
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                                              Gaps
                                                                                                                                                                          DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYCQNDHIYPYTFGGGTKLEIK 116
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  Length 113;
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                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10340189;
Publication No. US20030229207A1
GENERAL INFORMATION:
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSER MCANDYESSE:
STREET: 500 W. Madison Street, 34th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 11023US07 / 200-71.P2.C2
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
Score 541; DB 6; L
Pred. No. 6.6e-41;
4; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.4%; Score 536; DB 4; L
llarity 91.2%; Pred. No. 1.9e-40;
Conservative 3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/245,202A
FILING DATE: -UNKNOWN>
APPLICATION NUMBER: 08/082,842
FILING DATE: 23-JUN-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/340,189
FILING DATE: 10-Jan-2003
CLASSIFICATION: 530
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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ADDRESSEE:
STREET: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIVWIQSPSSLSVSAGERVIMSCKSSQSLLNSGNQKNFLAWYQQKPGQPPKLLIYGASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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    61 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHSYPLTFGAGTKLEIK 113
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APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 67
CORRESPONDER: ADDRESS:
ADDRESSEE: MCANdrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PLOPPY disk
COMPUTER: COMPATION:
COMPUTER: PROCESSION:
COMPUTER: PROCESSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels
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REPERENCED FOCKER: 32,918
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFRATION: 532/707-9880
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/11133775
; Publication No. US20050239141A1
; CSMERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/097,980
FILING DATE: 16-JUN-1998
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
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NAME: Janet M. McNicholas, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                   Sequence 2, Application US/10325696
Publication No. US20040005630A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 113 amino acide
TYPE: amino acid
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Matches 103; Conservative
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                                                                                                                             RESULT 7
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DEPLICANT: ImmunoGen, Inc.
TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
TITLE OF INVENTION: LEUKEMIA USING THE SAME
FILE REFERENCE: A8427
CURRENT APPLICATION NUMBER: US/10/700,632
CURRENT APPLICATION NUMBER: US 60/424,332
PRIOR FILING DATE: 2002-11-07
NUMBER OF SEQ ID NOS: 94
SOFFWARE: Patentin version 3.2
SEQ ID NO 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.4%; Score 536; DB 6; Length 113; 91.2%; Pred. No. 1.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11023US06/200-71.P1.C3
                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/133,775
E: McAndrews, Held & Malloy, Ltd.
500 West Madison Street, 34th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                 CUKKENI APPLICATION DATA:
CUKKENI APPLICATION NUMBER: US/11/133,775
FILING DATE: 19-MAY-2005
CLASSIFICATION D.:
APPLICATION NUMBER: US/09/097,980
FILING DATE: 16-JUN-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
PRIOR APPLICATION UNMBER: 08/107,669
FILING DATE: 13-AUG-1993
PRIOR APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-BC-1992
PRIOR APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-BC-1992
PRIOR APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-BC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Janet M. MCNICHOLAB, Ph.D.
REGISTRATTON NUMBER: 32,918
REGISTRATTON NUMBER: 32,918
REGISTRATTON NUMBER: 11023US06/20
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                  IL
: United States of America
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Publication No. US20050118183A1
GENERAL INFORMATION:
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Best Local Similarity 91.2<sup>3</sup>
Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                   Chicago
                                     STATE: IL
COUNTRY: Uni'
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US-10-144-644-46
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                                                                                                                                                                                                                                                 64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                                                                                                                                                                                                                             Sequence 46, Application US/10144644

Publication No. US2003005942941

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL S.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: McMillan, Lynette J.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
ITTLE OF INVENTION: Recombinant IL5 Antagonists Useful in ITTLE OF INVENTION: Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                     Query Match 88.4%; Score 536; DB 5; Length 115; Best Local Similarity 91.2%; Pred. No. 1.9e-40; Matches 103; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PULDASJITION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
FILING DATE: 06-JUN-1995
FILING DATE: 06-JUN-1995
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/467420
FILING DATE: 22-DEC-1994
ATTORNEY/AGENT INFORMATION: INFORMATION:
NAME: SULEON, J6ffrey, A.
REGISTRATION NUMBER: 34,028
REGISTRATION NUMBER: 34,028
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SmithKline Beecham Corp
STREET: P.O. Box 1539-UW2220
CITY: King of Prussia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/144,644
FILING DATE: 2002-08-08
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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                      TYPE: PRT
CORGANISM: Mus musculus
US-10-700-632-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
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US-10-144-644-46
; . LENGTH: 115
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                                                 Gaps
                                                                                                                                                                                  64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                                                                                          61 ESGVPDRFTGSGSGTDFTLTTSSVQAEDLAVYXCQNDYSYPFTFGSGTKLEIK 113
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Holmes, Stephen D.
McMillan, Lynette J.
Theisen, Timothy W.
TITLE OF INVENTION: Recombinent IL5 Antagonists Useful in
Treatment of IL5 Mediated Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/144,644
FILING DATE: 2002-08-08
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/363131
FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFERMATION:
    Length 113;
Score 535; DB 4; Length 11
Pred. No. 2.3e-40;
5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp
STREET: P.O. Box 1539-UW2220
CITY: King of Prussia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REPERENCE/DOCKET NUMBER: P50282-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-700-740-46
                                                                                                                                                                                                                                                                                                   RESULT 11
US-10-700-740-46
US-10-700-740-46
Sequence 46, Application US/10700740
Publication No. US20040156850A1
GENERAL INFORMATION:
APPLICANT: Appelbaum, Edward R.
Chaiken, Irwin M.
Cook, Richard M.
Cook, Richard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
    88.3%;
90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 76
  Query Match
Best Local Similarity 90.33
Matches 102; Conservative
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RESULT 13
US-10-144-644-16
  Query Match
Best Local S:
Matches 102,
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                                                                                                               4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63
                                                                                                                                                                                                                                                                   RESULT 12
US-11-076-395-46

Sequence 46, Application US/11076395

Publication No. US20060029594A1

GENERAL INFORMATION:
Appelbaum, Edward R.
Chainken, Irwin M.
Cook, Richard M.
Gross, Mitchell S.
Holmes, Stephen D.
MCMillan, Lynette J.
Theisen, Timothy W.
Theisen, Timothy W.
Treatment of IL5 Antagonists Useful in
                                              Gaps
                                                                                                                                                                                                  DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                              ;
0
Query Match 88.3%; Score 535; DB 4; Length 113; Best Local Similarity 90.3%; Pred. No. 2.3e-40; Matches 102; Conservative 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTER PENDABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PRIDK DATE: 09-Mar-2005
CLASSIFICATION NUMBER: US/11/076,395
PRIOR APPLICATION NUMBER: US/10/700,740
FILING DATE: 04-Nov-2003
APPLICATION NUMBER: US/10/144,644
FILING DATE: 04-Nov-2003
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/467420
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/467420
FILING DATE: 23-DEC-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corp
STREET: P.O. Box 1539-UW2220
CITY: King of Prussia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282-2
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                            4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR
                                               Gape
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                                                                                                                                                                                    64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
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Publication No. US2003005942941

GENERAL INRORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Cook, Richard M.
APPLICANT: Goos, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: Modillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.8%; Score 526; DB 4; Length 113; 89.4%; Pred. No. 1.5e-39;
Length 113;
                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 19406-0339
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parentin Release #1.0, Version #1.30
88.3%; Score 535; DB 6;
90.3%; Pred. No. 2.3e-40;
iive 5; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PATENTIN RELEGGG TO., CURRENT APPLICATION NUMBER: US/10/144,644
FILING DATE: 2002-08-08
CLASSIFFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467420
FILING DATE: 06-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGBNT INFORMATION: NAME: SULTON, JEffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: 950282-2
TELECPHONE: 610-270-5094
TELECPHONE: 610-270-5090
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp
STREET: D.O. Box 1539-UW2220
CITY: King of Prussia
STATE: Pennsylvania
                                               102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 89.4
Matches 101; Conservative
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TYPE: amino acid
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TOPOLOGY: linear
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                          Similarity
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1 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSGNQKNYLAWYQQKPGQPPKLLIYGASTR 60
                                                                   64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                                                                                                                                                                                                                                                     Gross, Mitchell S.
Holmes, Stephen D.
McMillan, Lynette J.
TILE OF INVENTION: Recombinant
                                                                                                                                                                                                                                                                                                    Appelbaum, Edward R.
Chaiken, Irwin M.
Cook, Richard M.
                                                                                                                                                                                                                  Sequence 16, Application US/11076395
Publication No. US20060029594A1
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 113 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FELEPHONE: 610-270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPOLOGY: linear
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                                                                     1 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSGNQKNYLAWYQQKPGQPPKLLIYGASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                             64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                   61 ESGVPDRFTGSGSGTDFTLSISSVQAEDLAVYYCONVHSFPFTFGSGTELEIK 113
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                                                                                                                                                                                                                                                                                                                                                                                                               Gross, Mitchell S.
Holmes, Stephen D.
McMillan, Lynette J.
Theisen, Timchy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
Treatment of IL5 Mediated Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 526; DB 4; Length 113; Pred. No. 1.5e-39; 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION DAIRS

APPLICATION NUMBER: US/10/144,644

FILING DATE: 2002-08-08

APPLICATION NUMBER: US 08/470110

FILING DATE: 06-JUN-1995

APPLICATION NUMBER: US 08/467420

FILING DATE: 06-JUN-1995

APPLICATION NUMBER: US 08/363131

FILING DATE: 23-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp
STREET: P.O. Box 1539-UW2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/700,740 FILING DATE: 04-Nov-2003 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: P50282-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-700-740-16
                                                                                                                                                                                                         RESULT 14
US-i0-700-740-16
i Sequence 16, Application US/10700740
i Publication No. US20040156850A1
i GENERAL INFORMATION:
i APPLICANT: Ames, Robert S.
i Cook, Richard R.
Chalken, Irwin M.
Cook, Richard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAMB: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 113 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 610-270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: King of Prussia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 89.4%;
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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61 ESGVPDRFTGSGSGTDFTLSISSVQAEDLAVYYCQNVHSFPFTFGSGTELEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IL5 Antagonists Useful in
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MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: POC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/076,395

FILING DATE: 09-Mar-2005

CLASSIFICATION **CUNKNOWN>

PRIOR APPLICATION NUMBER: US/10/700,740

FILING DATE: 09-00-2003

APPLICATION NUMBER: US/10/144,644

FILING DATE: 06-JUN-1995

APPLICATION NUMBER: US 08/470110

FILING DATE: 06-JUN-1995

APPLICATION NUMBER: US 08/467420

FILING DATE: 06-JUN-1995

APPLICATION NUMBER: US 08/363131

FILING DATE: 23-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: SURLON, UMBER: 34,028

REGISTRATION NUMBER: 34,028

REFERENCE/DOCKET NUMBER: P50282-2

TELECOMMINICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treatment of ILS Mediated Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 113;
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Best Local Similarity 89.4%; Pred. No. 1.5e-39;
Matches 101; Conservative 5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
RADDRESSEE: SMitchKilne Beecham Corp.
STREET: P.O. Box 1539-UW2220
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-11-076-395-16
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4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63

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1 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSGNQKNYLAWYQQKPGQPPKLLIYGASTR 60
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GGGTKLEIK 116	GSGTELEIK 113
SGTDFTLTISSVQAEDLAVYYCQNDHIYPYTF	SVQAEDLAVYYCONVHSFPFTF
64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116	61 ESGVPDRFTGSGSGTDFTLSISSVQAEDLAVYYCQNVHSFPFTFGSGTELEIK 113
64	61
ò	Db

Search completed: May 19, 2006, 17:52:58 Job time: 116.159 secs

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TYPE: PRT
ORGANISM: Artificial Sequence
RESULT 1
US-11-075-891-26
FEATURE:
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71, Appl
91, Appl
72, Appl
92, Appl
2965, Ap
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/EMC Celerra SIDS3/ptodata/2/pubpaa/US09_NEW PUB.pep:*
/EMC Celerra SIDS3/ptodata/2/pubpaa/US06_NEW PUB.pep:*
/EMC Celerra SIDS3/ptodata/2/pubpaa/US07_NEW PUB.pep:*
/EMC Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/EMC Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/EMC Celerra SIDS3/ptodata/2/pubpaa/US10_NEW PUB.pep:*
/EMC Celerra SIDS3/ptodata/2/pubpaa/US11_NEW PUB.pep:*
/EMC Celerra SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                       May 19, 2006, 17:49:02 ; Search time 5.52381 Seconds (without alignments) 44.858 Million cell updates/sec
                                                                                                          1 SRGDIVMTQSPSSLSVSAGE......CQNDHIYPYTFGGGTKLEIK 116
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26,
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        GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-219-563-91
US-11-219-563-92
US-11-219-563-92
US-11-219-92-33
US-11-221-902-23
US-11-221-902-13
US-11-221-902-13
US-11-221-902-17
US-11-221-902-17
US-11-221-902-17
US-11-221-902-17
US-11-221-902-17
US-11-221-902-17
US-11-221-902-17
US-11-221-902-17
US-11-221-902-18
US-11-221-902-18
US-11-251-91-18
US-11-075-891-18
                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                    21570 segs, 2136119 residues
                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                        protein search, using sw model
                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                      seq length: 0
seq length: 200000000
                                                                                         US-09-889-936A-8
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Match Length
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4, 1
115, 1
13, 1
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68,
48,
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Publication No. US20060088521A1

GENERAL INFORMATION:

APPLICATION NO. US20060088521A1

TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT

PILE REFERENCE: 283922U896

CURRENT APPLICATION NUMBER: US/11/075,891

CURRENT FILING DATE: 2005-03-10

PRIOR PILING DATE: 2005-03-7

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PATENTIN NOS: 36

SOFTWARE: PATENTIN NOS: 36

LENGTH: 118
                                                                                               Sequence - 
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Sequence
Sequence
Sequence
Sequence
Sequence
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Sequence 71, Application US/11219563

Publication No. US20060088539A1

GENERAL INFORMATION:

APPLICANT: Bander, Neil

TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF

TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF

FILE REFERENCE: 13651.001 (BZL-001)

CURRENT APPLICATION NUMBER: US/11/219,563

CURRENT FILING DATE: 2005-09-02

PRIOR APPLICATION UNMBER: PCT/US04/06586

PRIOR FILING DATE: 2004-03-03
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88.4%; Score 536; DB 7; Length 118;

Best Local Similarity 91.2%; Pred. No. 8e-25;

Matches 103; Conservative 3; Mismatches 7; Indels
                        US-11-239-308-6
US-11-219-563-66
US-11-075-891-12
US-11-075-891-16
US-11-075-891-16
US-11-075-891-16
US-11-219-563-63
US-11-254-182-3
US-11-254-182-15
US-11-254-182-15
US-11-254-182-15
US-11-254-182-15
US-11-254-182-15
US-11-254-182-15
US-11-254-182-17
US-11-254-182-17
US-11-219-563-50
US-11-219-563-50
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US-11-211-917-48
US-10-981-300-10
US-10-981-300-21
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Query Match
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Publication No. US20060088539A1

GENERAL INFORMATION:

APPLICANT: Bander, Neil

TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF

TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF

FILE REFERENCE: 13651.001 (BZL-001)

CURRENT APPLICATION NUMBER: US/11/219,563

CURRENT APPLICATION NUMBER: US/11/219,563

PRIOR PILING DATE: 2005-09-02

PRIOR FILING DATE: 2004-03-03

PRIOR FILING DATE: 2003-03-03

PRIOR FILING DATE: 2003-03-03

PRIOR PLICATION NUMBER: 10/449,379

PRIOR FILING DATE: 2003-03-03

NUMBER OF SEQ ID NOS: 144

SOFTWARE: FREUESEQ FOR Windows Version 4.0

SOFTWARE: FREUESEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 85.1%; Score 516; DB 7; Length 113; Best Local Similarity 88.5%; Pred. No. 9.8e-24; Matches 100; Conservative 4; Mismatches 9; Indels
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Sequence 72, Application US/11219563

PUBLICATION NO. US20060088539A1

GENERAL INFORMATION:
APPLICANT: Bander, Neil

TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
FILE REFERENCE: 13551.001 (BZL-001)
CURRENT APPLICATION NUMBER: US/11/219,563
                                                                                                                                                                                                                                                                               Length 113;
                                                                                                                                                                                                                                                                                                                       9; Indels
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Pred. No. 9.8e-24;
4; Mismatches 9;
PRIOR APPLICATION NUMBER: US 10/379,838
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 10/449,379
PRIOR FILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 71
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 88.5%;
Matches 100; Conservative
                                                                                                                                                                                     TYPE: PRT
CORGANISM: Mus musculus
US-11-219-563-71
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US-11-219-563-91
                                                                                                                                                                LENGTH: 113
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TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
FILE REPERBORE: 13651.001 (SEL-001)
CURRENT APPLICATION NUMBER: US/11/219,563
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: PCT/US04/06586
PRIOR APPLICATION NUMBER: US 10/379,838
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 10/449,379
PRIOR APPLICATION NUMBER: 10/449,379
PRIOR FILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FASCESEQ for Windows Version 4.0
SEQ ID NO 92
LENGTH: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 113;
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79.6%; Pred. No. 3.4e-21;
tive 10; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 483; DB 7;
Pred. No. 6.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Mismatches
CURRENT FILING DATE: 2005-02
PRIOR APPLICATION NUMBER: PCT/US04/06586
PRIOR FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: US 10/379,838
PRIOR PLING DATE: 2003-03-03
PRIOR PLING DATE: 2003-03-03
PRIOR PLING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: majority sequence US-11-219-563-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: majority sequence US-11-219-563-92
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; Sequence 92, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 81.4%;
Matches 92; Conservative
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Matches 90; Conserva
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US-10-511-937-2965
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APPLICANT: Wyeth
TITLE OF INVENTION: HUMANIZED ANTI-574 ANTIBODIES AND ANTI-574/CALICHEAMICIN CONJUGATE
FILE REFERENCE: 040000-0317285
CURRENT APPLICATION NUMBER: US/11/221,902
CURRENT FILING DATE: 2005-09-09
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.3
SEQ ID NO 2.3
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TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGATIFLE FILLE REFERENCE: 040000-0317285
CURRENT APPLICATION NUMBER: US/11/221,902
CURRENT APPLICATION NUMBER: US/11/221,902
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.3
SOFTWARE: Patentin version 3.3
LENGIH: 214
TYPE: PRT
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                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                               64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
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                                                                                                                                          17; Indels
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                                                                              Query Match

72.9%; Score 442; DB 7;
Best Local Similarity 75.2%; Pred. No. 1.2e-19;
Matches 85; Conservative 11; Mismatches 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.0%; Score 412; DB 7; 71.7%; Pred. No. 5.2e-18;
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NORME/KEX: MISC_FEATURE
LOCATION: (1)..(107)
OTHER INFORMATION: light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Mismatches
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; Sequence 23, Application US/11221902
; Publication No. US20060088522A1
; GENERAL INFORMATION:
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Best Local Similarity 71.79
Matches 81; Conservative
; ORGANISM: Homo sapiens
US-11-254-679-5
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TYPE: PRT
ORGANISM: Artificial
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APPLICANT: Will Herren
APPLICANT: Will Herren
APPLICANT: Milan, Christian
APPLICANT: Gao, Changshou
APPLICANT: Gao, Changshou
APPLICANT: Allan, Ling-Ling
APPLICANT: Kiener, Peter
APPLICANT: Mao, Su-Yau
APPLICANTON: High Affinity Antibodies Against HMGB1 and Method of Use Thereof
FILE REFERENCE: HB601US
CURRENT FILING DATE: 2005-10-21
PRIOR PELING DATE: 2005-01-10-22
PRIOR PELING DATE: 2005-03-10
PRIOR APPLICATION NUMBER: 60/662,944
PRIOR FILING DATE: 2005-03-18
PRIOR PILING DATE: 2005-03-18
PRIOR FILING DATE: 2005-03-18
PRIOR FILING DATE: 2005-03-18
PRIOR FILING DATE: 2005-03-09
PRIOR FILING DATE: 2005-03-09
NUMBER OF SEQ ID NOS: 103
SOFTWARE: Patentin version 3.3
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APPLICANT: Ly, NGGC;
APPLICANT: Prentice, James
APPLICANT: Prentice, James
APPLICANT: MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 50661200104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT APPLICATION NUMBER: PCT/US2003/012946
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/135,899
PRIOR APPLICATION NUMBER: US 10/325,899
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77.2%; Pred. No. 3.5e-20;
tive 10; Mismatches 15
                                                   APPLICANT: EXPRESSION DIAGNOSTICS, INC.
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Publication No. US20060099207A1
GENERAL INFORMATION:
. Publication No. US20060088836A1
                                                                                                            Fry, Kirk
Woodward, Robert
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Best Local Similarity 77.2%
....hem 88; Conservative
                                                                              Wohlgemuth, Jay
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; ORGANISM: Homo sapiens
US-10-511-937-2965
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICARY: Wyeln

TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGATE

CURRENT APPLICATION NUMBER: US/11/221,902

CURRENT PELING DATE: 2005-09-09

NUMBER OF SEQ ID NOS: 89

SEQ ID NO S: 89

SEQ ID NO S: 80

LENGTH: 214
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TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGATE
TITLE OF INVENTION: 040000-0317285
CURRENT APPLICATION NUMBER: US/11/221,902
CURRENT APPLICATION DATE: 2005-09-09
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: artificial sequence is derived from mouse and human antibody US-11-221-902-17
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                                                                                                                                                                                                       66.7%; Score 404; DB 7; Length 101; 76.2%; Pred. No. 1.4e-17; Live 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.5%; Score 391; DB 7; Length 107; 69.0%; Pred. No. 7.4e-17; ive 13; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                      64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYP 104
                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 17, Application US/11221902; Publication No. US20060088522A1; GENERAL INFORMATION:
PRIOR FILING DATE: 2002-10-09
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 69.01
Matches 78; Conservative
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                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Artificial
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ORGANISM: Artificial
FEATURE:
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US-11-221-902-5
                                                                                       LENGTH: 101
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Matches 7
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Sequence 63, Application US/11221902
Sequence 63, Application US/11221902
Publication No. US20060088522A1
GENERAL INFORMATION:
APPLICAMT: Wyeth
TITLE OF INVENTION:
FILE REFRENCE: 040000-0317285
CURRENT APPLICATION NUMBER: US/11/221,902
CURRENT PILING DATE: 2005-09-09
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.3
SEQ ID NO 63
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Publication No. US200600888331
GENERAL INFORMATION:
APPLICANT: Smider, Vaughn
APPLICANT: Larrick, James W.
APPLICANT: Integrigen, Inc.
ACURRENT APPLICATION NUMBER: US/11/239, 308
ACURRENT APPLICATION NUMBER: US/10/683, 733
APRIOR FILING DATE: 2003-10-09
PRIOR PILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: US 60/417, 979
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8.2e-18;
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Best Local Similarity 71.7%;
Matches 81; Conservative 1.
                                                                                       FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (50)...(56)
OTHER INFORMATION: CDR 2
                                                 LOCATION: (24)..(34)
OTHER INFORMATION: CDR 1
                                                                                                                                                                                                                       ) OTHER INFORMATION: CDR3 US-11-221-902-11
                     NAME/KEY: MISC_FEATURE LOCATION: (24)...(34)
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT
FILE REFERENCE: 040000-0317285
CURRENT APPLICATION NUMBER: US/11/221,902
CURRENT FILING DATE: 2005-09-09
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.3
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TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT
FILE REFERENCE: 040000-0317285
CURRENT APPLICATION NUMBER: US/11/221,902
CURRENT FILING DATE: 2005-09-09
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.3
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OTHER INFORMATION: artificial sequence is derived from mouse and human antibody OTHER INFORMATION: sequences
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                                                                                                                                                                                     Length 214;
                                                                                                                                                                                                                                  16; Indels
                                                                                                                                                                                Query Match 64.5%; Score 391; DB 7; Best Local Similarity 69.0%; Pred. No. 1.2e-16; Matches 78; Conservative 13; Mismatches 16
                                                                                     ; LOCATION: (1)...(107)
; OTHER INFORMATION: light chain variable region US-11-221-902-5
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NAME/KEY: MISC_FEATURE
NAME/KEY: (1). (107)
OTHER INFORMATION: light chain variable region
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Publication No. US20060088522A1
GENERAL INFORMATION:
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Publication No. US20060088522A1
GENERAL INFORMATION:
                                             NAME/KEY: MISC FEATURE ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial
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US-11-221-902-9
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TYPE: PRT

| CORGANISM: Artificial
| FEATURE:
| COTHER INFORMATION: artificial sequence is derived from mouse and human antibody
| COTHER INFORMATION: artificial sequences
| COCATION: (1)...(107)
| COCATION: (1)..
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